

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: I.N.S.E.R.M
- (B) STREET: 101, rue de Tolbiac
- (C) CITY: PARIS CEDEX 13
- (E) COUNTRY: FRANCE
- (F) POSTAL CODE (ZIP): 75654

(ii) TITLE OF THE INVENTION: DNA, specific proteins and peptides of the *Neisseria meningitidis* species bacteria, methods for obtaining them and their biological applications.

(iii) NUMBER OF SEQUENCES: 99

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (OEB)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GATCCGCTGC CGGCAGACGA ATATCAAGAC ATCTTCGATT TTATGAAACA GTATGACTTG 60  
 TCTTACCCGT ATGAATATCT GCAGGATTGG ATAGATTACT ATACGTTCAA AACCGATAAG 120  
 CTGGTATTTG GTAACGCGAA GCGAGAGTGA GCCGTAAAAC TCTGAGCTCC TGTTTTATAG 180  
 ATTACAACCTT TAGGCCGTCT TAAAGCTGAA AGATTTTCGA AAGCTATAAA TTGAAGCCCT 240  
 TCCACAGTAC ATAGATC 257

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GATCATGTTC AAATAGATAG GCATGGGAAG CTGCAGCTCT AACGTCCATG AAAATATGTT 60  
 GCATAGCTGC AAGCGGAACG CCTTTTCTTT CATCTACATA ATCTATAGAG TCAAGGCAAC 120  
 CGCTATTGAA ATTAGCAGTA TTGCCTATGA TTACATTAGT AATATGCTCA TACCATTTTT 180

GGGTGGTCAT CATATTGTGC CCCATTGTGA TCTCCTTATA TTGGTTTTAG AAGGAACTTT 240

GACAGGAAGA ATAACGGCCT TACCTGTTTG ACGATC 276

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GATCTGGTGG TGTTTGCACA GGTAGGCGCA TACTTGTTTCG GGACTGAGTT TGCGGCGGAT 60

AAGGGTGTCG ATGTGCTGAA TCAGCTGCGA ATCGAGCTTA TAGGGTTGTC GCTTACGCTG 120

TTTGATAGTC CGGCTTTGCC GCTGGGCTTT TTCGGCGCTG TATTGCTGCC CTTGGGTGCG 180

GTGCCGTCTG ATTTGCGCGC TGATGGTGCT TTTGTGGCGG TTAAGCTGTT TGGCGATTTT 240

GGTGACGGTG CAGTGGCGGG ACAGGTATTG GATGTGGTAT CGTTCGCCTT GGGTCAGTTG 300

CGTGTAGCTC ATGGCAATCT TTCTTGCAAG AAAGGCCGTA TGCTACCGCA TACTGGCCTT 360

TTTCTGTTAG GGAAAGTTGC ACTTCAAATG CGAATCCGCC GACCTCTTTC AGTTACAGCA 420

GCTTGATC 428

(2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATCCTGCAT TGACATCGGC CTTGGCTGTC AGGGTATTGT GACCGGTAAA GTCGGCATT 60  
 CCGTTGGCCA ATAAGGATAC ATGACCGTCT GCAGAAACAG CATGAAGGCC GTCTGAAACG 120  
 ATATTGCCCT GCAATGCGGT GGTTCGAGA GCCTTGGCTG CGTTCAGCTT GGTATTGCGA 180  
 AGCTGAATAT TGCCTTTGGC TGCCTGAATG TGCAGATTAC CCGAGTTGGT ACGCAGATTG 240  
 GTATTGGTAA CATTGAGCAA GCCTGCCTCC ACACCCATGT CTTTGTAGGC AGTGAGGGTT 300  
 TTACTGGTGC CGGTAATATG GGCAGCGTTA TCCGATTTC AATGGATGCT GGCCGGCAGA 360  
 CAAATCTTTA TCAACATTCA AATTCAGATC 390

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GATCAGATTG GTGAAGACGG TATTACCGTC AATGTTGCAG GCCGTTCTGGG ATATACGGCG 60

AAAATCGACG TGTCTCCGAG TACCGATTTG GCGGTTTATG GCCATATTGA AGTTGTACGG 120

GGTGCAACGG GGTGACCCA ATCCAATTCA GAGCCGGGTG GAACCGTCAA TTTGATC 177

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GATCAATGAT GCTACTATTC AAGCGGGCAG TTCCGTGTAC AGCTCCACCA AAGGCGATAC 60

TGAATTGGGT GAAAATACCC GTATTATTGC TGAAAACGTA ACCGTATTAT CTAACGGTAG 120

TATTGGCAGT GCTGCTGTAA TTGAGGCTAA AGACACTGCA CACATTGAAT CGGGCAAACC 180

GCTTTCTTTA GAAACCTCGA CCGTTGCCTC CAACATCCGT TTGAACAACG GTAACATTAA 240

AGGCGGAAAG CAGCTTGCTT TACTGGCAGA CGATAACATT ACTGCCAAAA CTACCAATCT 300

GAATACTCCC GGCAATCTGT ATGTTTCATAC AGGTAAAGAT C

341

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GATCCAAC	TG	TTTGATT	TTTA	CTGGCT	GCTT	CTCCAT	GCGC	GGTATT	GACC	AAAGCC	GCAA	60
GGATATT	CGC	TTCCAG	ATTG	TCTTTC	CAGG	TGCCGC	CGGT	GACAGC	GGTA	TTAATC	CAGT	20
CGGCACT	GCC	CGCATT	GGCT	AGGTTG	ACGG	TCAGGT	TGTT	GATC				164

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATCAATCAC ACATCTTGTC ATTTTTCGA TTCCTTCATT TCGGTTTCTA ATGTTTCAAT 60  
 TCTTGCGGCC ATTTCTGAA TGGCTTTAGT CAAAACGGGG ATGAACGCTT CGTATTGAC 120  
 GGTGTAGGTA TCGTTTGTTC TATTTACCAT CGGCAATCGA CCATATTCAT CTTCCAGCGC 180  
 AGCAATGTCC TGGGCAATAA ACCAATGCCG CAACCGATC 219

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATCTTGGGT AAGCCCCAA CCTGCATAGA AAGGCAGGCC GTAGCAGCTG ACTTTTTTGC 60  
 CGCGCAACAA GGCTTCAAAA CCGGTCAGCG AAGTCATGGT ATGTATTTTCG TCTGCGTATT 120  
 GGAGACAGGT CAGGATGTCG GCTTGTTTCGG CGGTTTGGTC GGCATATCGT GCAGCATCAT 180  
 CAGGGGAAAT ATGGCCGATG CGGTTACCGC TGAATACATC GGGATGCGGT TTGTAGATGA 240  
 TATAGGCATT GGGGTTTCGT TCGCGTACGG TACGGAGCAA ATCCAGATTG CGGTAGATTT 300  
 GGGGCGAACC GTAGCGGATA GACGCATCAT CTTCAACCTG GCCGGGAACG AGGATC 356

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GATCCGCTTT CAGTTTCCGT ACCGGTGGCA TCAGTCAAGT CCGTTTTGTG CACCAAACCG 60

CGTCCATATG AAACATAAAA CAAATCGCTT AAGCCCAAAG GGTTATCGAA CGATAAAGCG 120

ACATTTTCCTT GATATTTGCC GGTCGTTTTG CCGCCCGCAT CATCTATAACC GATACTGAAC 180

CGTATGGGTT TATTCTGCTG CCATTGATC 210

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GATCCCGAAA CGCAATTGGT CGAAAGCTAT ATGCTGAACG ATGTGTTGCG GTTTTGGGAC 60

AGCGCAGGTT TGGGCGATGG GAAAGAAGCC GACCGCGCCC ATCGGCACAAA ACTGATTGAT 120

GTCCTGTCTA AAACCTATAC TCATTCGGAT GGGCAGTGGG GCTGGATAGA TTTGGTGTTC 180

GTTATCCTTG ACGGCAGCTC CCGCGATTTC GGTACGGCCT ATGATTTGTT GAGGGATGTT 240

ATCCTTAAAA TGATTGATC 259

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GATCAAATGG ATGATTTATA TAGAATTTTC TTTTACGACT GCGTGCCGTT TGAAAAGAAA 60

ATGCACAATC CCGTATCTCA TCGTGCCATA GATTTTTCAA AGACTCCGGA AGCCATATTT 120

CGTTGCAATC TGCATACCGA ATTGAAGAAG AAGCGTAAAT TAGCGTTACG TTTAGGCAAG 180

CTGTCGGACA ATACAGCATG GATATTAAAA CCCCAAGTCA TGAAAAATCT TCTGAAAAAC 240

CCGTCAACTC AAATTACGGA AAACGATGTC GTGCTCGATG TTAAACAAAA AGGTGTAGAT 300

ATGCGTATAG GCTTGGATAT TTCATCTATT ACCTTAAAAA AACAAGCCGA TAAAATCATC 360

TTGTTTTCTG GTGATTCCGA TTTTGTCCCA GCAGCCAAAT TAGCCAGACG GGAAGGTATC 420

GATTTTATTC TTGATC 436

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GATCGTTTTA CGTCGCAATC GAGCTTTGTG GTGCGCTCGC CTAAAGCCA ATCTTCTCTC 60

AATGGCCTGG GTGCCATTTT GCAGGGCACA GGTTTTGCCG GTGCGCAAGA CGATATTTAT 120

ACCGTGCAGG AATATATGCA GTCGCGTTCG GCTTTGGATG CGTTGCGTAA GAAAATGCCC 180

ATTCGCGATT TTTATGAAAA AGAAGGCGAT ATTTTCAGCC GTTTTAATGG TTTTGGCCTG 240

CGTGGCGAGG ATGAGGCGTT TTATCAATAC TACCGTGATA AGGTATCCAT CCATTTTGAC 300

TCTGTCTCAG GCATTTCCAA TTTGAGCGTT ACATCGTTTA ATGCCGGTGA ATCTCAAAAAG 360

ATC 363

(2) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GATCTTGCGT CATTATATC TTCACCGATA TTGCAATTAC CGCCGTTCCA GTTGAAATAA 60  
 CAACGACTAA AATTGTAGTT CCTAAAAGAA TCATTCCTAT TCTTGCGTAC CATTTCCTAA 120  
 TAATTGCGCC CGACAATTTT CATTTAATGC TCCATCAGTT CTTTACTTC CGGAAATCTG 180  
 CTGTAATCTG ACATAAGACG CATAATTGAA CTATCAACGC CGTAACAGCC ATAGGTTTTA 240  
 ATACCGTTTT CGGCGTGTTT CCAAATGCAA TTACTGTATT CGTAGCCTTT TACAAATTTA 300  
 TCGGTTTCGG GATC 314

## (2) INFORMATION FOR SEQ ID NO: 15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCATACGA ATCTACCCTA AAATACCCCG TCGCCGATTT AGGATTGGCT ACATAAAGCT 60  
 CATTATAAGG GTATTTTGAT GACATGATAC GGTTAAATTC ATTGCCGTTG TTTATCCTGA 120  
 TTCTATAAAT TGGTTCAACA GCAAAGCCTC TGGATTCCCT TAATTGATTA TAATATTGCC 180  
 TGTATGTTTG TACATCATGT CTTGTCCACG GCTCTCCAGG AGTCCTCAGA ATAGCAATCC 240  
 CGTTAAATTT CGGATC 256

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GATCCACGCC TGTGCCTACC TTGGCTTTTT GTTCGCCAAA CAAGGCATTT AAGGTTGAGG 60  
 ACTTGCCGAC ACCTGTCGCA CCGACAAGCA AGACATCCAA ATGACGGAAA CCGGCTGCTG 120  
 TGACTTTTTG CCCGATTTC AAAATACGGT AACGATGCAT ATGCGCTCCT ACCAGCCAAA 180  
 AAAAGAAGCA ACCGTGCTAA TCGCCCCTCC AATCGCTTTT GCAGCACCGC CGATC 235

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GATCCAACGG GCATCGCTGT CCTACTCGG TGTGGTTTGA CCGCTGATTT GTCCTTCTTC 60  
 GTCAACTTCT ATGGCCTGAC GCTGTTTGCT GCCGGCGGTC TGGATAATGG TGGCATCAAC 120  
 GACGGCGGCG GATGCTTCT CTATTTTCTAG GCCTTTTCTG GTCAGTTGGC AGTTAATCAG 180  
 TTTGAGTAAT TCGGACAGGG TGTCGTCTTG CGCCAGCCAG TTGCGGTAGC GGCATAAGGT 240  
 ACTGTAATCG GGGATGATC 259

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```
GATCTGTGCC GTTGATTTTA TCTTTCAGAT GCAGCATCGA ATATCGGAAA GCCAAATCAG      60
CAATTCTTTT TGCATCGTGT GGATTTTGAG ACGGGCCTAA TGACCGTACC CGCTTAATAA      120
AAAATGCACC GTCAATCAAA ATGGCGGTTT TCATATTGCT TCCCCTATAT TTGTCAAAGA      180
TATAAAAAAG CCCTTGGGAT C                                                  201
```

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```
AATTCAAAGG AGGCATTTGT TGCAAGAAAA GTACAAAGTG ATTTGCAAAA AGCATTGAAT      60
GCTAGCAACT ATAACAAGCA GCAATATGCA AGACGTGCGG CAACAGCGTT AGAGAATGCT      120
TCAAAATCAA AAGTTATGGC AGCGAATTCT TTTTGATCTA TCTTGTGCGA ACGGGTCAAA      180
TATTCTTCGT ACATTGAGTT AATCGTACCA ATCGCCCTAA CCACATTTTC ATCAGAAAAT      240
ATGGAAATAA TAGCATCCCT ATACGCACCT AGTGTAATAT TGTTTCTATT ATTAGTTATA      300
```

GCATTATTCG AATACATAAT AGCACCTCCA AATT

334

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AATTCCTGCG CACCTTTGCC GATGGGGAGA TAATCGCCTT TTTGCAGCAT TCTGCCCTGA 60

TGGCCGCCGA AACCGGCTTT CAGGTCGGTA CTTCTCGAAC CCATCACTTC CGGCACATCA 120

AATCCGCCCCG CCACGCACAC ATAGCCGTAC ATGCCCTGCA CGGCACGCAC CAGTTTCAAG 180

GTCTGCCCTT TGCGGGCGGT ATAACGCCAA TACGAATAGA CCGGTTTCGCC GTCCAATT 238

## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AATTGGGCGA GATGCTGCCG GAAACGGATT TAAACAGAT TCGGGCGGCA GTGTTGAAGA 60  
 CGAACGATGA GGCGGCATTG CAGAAGGTGG TGAAAACGGC CAAAGGCAAT GCGCGGAAAC 120  
 TGTCGAAGCT GCTGCTGATT GTGGACTATT TGTTCAGGT TAACCCTGAT GTTGATTTGG 180  
 ATGATGATGT AATCGAACAC GCGGAAACCT ATTTAATCCA CTAAACCTTT GACAGATAAG 240  
 GCAATAATT 249

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AATTTATGTA CGGTTTTGCC GTTTGCAGTC AGCCAGTCGG CAAGGCGCAG AAAAAATCG 60  
 CCGACAGGGC CTTGAAGCAG CAGGATATTT TCTGCGCTTT CAAGCAGGTT TTGCAGGTTA 120  
 TTTTGTAGGA CGGTCTGTTT CATGTTGCAA TGTGGTTTTG TTTTATATGT AATAGTTTTA 180  
 GGTGAACTT TCAAGCATAC GCCAAGAGAA TT 212



## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AATTCAGTGC CTGCGTCATA TCACGGCTAC CTTGTGGTTC AGGGTTACTG TATCGCCCCG 60  
 GGCATCGACG GCTTCAATAT GCAGCTTCAG CCAGCCGTGC TCGGGGGCGG ATGCGGTAC 120  
 TTGGATGGAT TGGGCGCGTT TGGACTGAAT CACGGGCTGC AAGGCTTGCT CGGCGTACTG 180  
 TTTGGCCAGT ACTTCGATGC GCTTTAAATG CTTTGGCGG CGCAATT 227

## (2) INFORMATION FOR SEQ ID NO: 24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GATCCAGGAC TCAAAAACCG ATTCCTAAT AGAGTGTCTA ATATCCCAAT CTTTTTTACC 60  
 CCCTCTGCTG TAGAATTGAT AGAGAAAGTT TGTCTATCTT TTTCATATAC CCATGCCTTC 120  
 TTTTATCAT TGTAGCTAAC ATAACCGCCA AACAATGCTT CTAGATC 167

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AATTCTTGCG GCCATTTCTT GAATGGCTTT AGTCAAAACG GGGATGAACG TTTCGTATTC 60  
 GACGGTGTAG GTATCGTTTG TTTTATTTAC CATCGGCAAT CGACCATATT CATCTTCCAG 120  
 CGCAGCAATG TCCTGGGCAA TAAACCAATG CCGCAACCGA TCTTCTTTAT GACTGCCGTC 180  
 CTTGATTGGA TTCGCCCACC ATTCGCGGAC TTTGTCCGCT CGTTCATCTG CCGGCAAGTC 240  
 TTTGAATAAT T 251

## (2) INFORMATION FOR SEQ ID NO: 26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs

- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

AATTCCCGAC TATCGCGGAT GCGTAGTTTT TGCCGGTGGG CAAGAGCAGG TGTGGGATAA	60
GTTAGGTGAT TTGCCCCGATG GCGTCAGCCT GACCCCGCCT GAATCGGTAA ATATTGACGG	120
CTTAAAATCC GTAAAACTCG TCGCATTAAA TGCTGCCGCT CAGGCTTTTA TTAACAAGCA	180
CGCCGGTATC GACAGCGTAC CTGAATT	207

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

AATTGTTTGG GAATAATCCA AACAAACAGC ATCAGGATAG CGGCGGCGGT CAGGCTGCCT	60
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GAAAGGATTT TGCCGGGGTT TTTTGTAGGC AAAGCGGACG AGAAACCAAA GCAACAGCAG 120  
 CATGGTGTCC CAATAGCCGA TTGAGAATAG GATGGCCAAA CCTTCTAGGA AATGGCGTAA 180  
 ATCGTTTGTG GTAACCATGG GTAGTTCCTG TGGTTAAATG TGCAGGCTGC TTTTGGCCGA 240  
 ACCTTGCCGC ATCTCAAAAG CAGCCTGCGC TTCAGCGTTG CGTTACGCAG TAAAATAATG 300  
 AATATTTGTA ACGGCTTGGG TATTTTTTGT CAATATTCCC GCCCTTCCCT TAACAGCTGC 360  
 CGCGCTTTCC GTTAAAATT 379

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

AATTCGCCGA AATCAGGCTG CTGCTCGATA ATCGGCGCGG CCGATTGGCG TTGTGCCTCG 60  
 ATTAAATCCA TCTTGTCTTG CAGACGTTTG GCCTGGCCTT TGCGGCGGCG TTCGGCCAGT 120  
 TGTTCATCC GCGTTTCCGC AAATGCCGCC CGTTTGTGTC CGTTGAATAC CGCTTTGCAA 180  
 ATCACCTTGC CCTGCATATC CTTACAATC ACATGGTCGG CATCGTGGAT GTCGTAAGCC 240  
 ACCCGTACCT TCTGACCGCT GTAATCCAGC AATT 274

## (2) INFORMATION FOR SEQ ID NO: 29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AATTCCGTTT TTATTGGGCT TTTTCCATCC ATCGGGTATG CCTGAAGGGA ACGCAAACCC 60  
 TGCCACTTGC CCATCGCTCC ATTCCCGCAT TAGCGCGTCT GACGGCAAGT GTTCTCGCGC 120  
 CCAATCAAGC CACGCCTGCC GCATTGCGGC CTTGTCCTGC TGAAAACTTC GCAGTGCTTT 180  
 TGCAACCGGC CCATCATTA CTTCAATCAA ATAAATCATT ATATTGCGT TCATTTTTC 240  
 TACACCTTCG CCACATCCAA ATT 263

## (2) INFORMATION FOR SEQ ID NO: 30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

AATTGTTCAA GAAAAAAGTC GGCACGGCGC GGCAACGGGG AAAATGCGTT GACGCCGTCT 60  
 TTTTCTAAGG TGATGTAGTA GGGGCGGAAA TAGCCTTCTT CAAACGCCCA GAAACTGGCT 120  
 TGGTTTTTCGT TTGCAATGCG TTTTGCAATG ACGTGATAAG GCGGTGTGTC GCCAAAGCAG 180  
 ACAACGGCCT GGATGTGATG TTGAGTGATG TATTCTTGCA AAAACTCAGG AAAGGCGTCG 240  
 TAGTTGTCGT TAAAAACAAC GGTATGCGCT TGAGTGGGCG GATAAAAATA GTCGTCGCCT 300  
 GCATTAAAGT TGAATT 316

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AATTCAATCA ACGGAAAACA CATCAGCATC AAAACAACG GTGGTAATGC CGACTTAAAA 60  
 AACCTTAACG TCCATGCCAA AAGCGGGGCA TTGAACATTC ATTCCGACCG GGCATTGAGC 120  
 ATAGAAAATA CCAAGCTGGA GTCTACCCAT AATACGCATC TTAATGCACA ACACGAGCGG 180

GTAACGCTCA ACCAAGTAGA TGCCTACGCA CACCGTCATC TAAGCATTAC CGGCAGCCAG 240  
 ATTTGGCAAA ACGACAAACT GCCTTCTGCC AACAAGCTGG TGGCTAACGG TGTATTGGCA 300  
 CTCAATGCGC GCTATTCCCA AATT 324

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AATTATGCAA AAAAACGCAA CGCCGAAAAA CTGGCACCGC GCGGATATTG TTGCTGCTTT 60  
 GAAAAAGAAA GGCTGGTCAC TTCGAGCACT TTCAATAGAA GCGGGGTTGT CGCCGAATAC 120  
 GCTTAGAAGC GCACTGGCCG CCCCTTATCT TAAGGGAGAA AGGATTATTG CCGCTGCAAT 180  
 CGGAGTGGAA CCGGAAGAGA TTTGGTCCGA ACGGTATGCA GATCGGAATT 230

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

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AATTTAATCG GTGGAATGCC TGTTCACCG CACCAATCCC GCTGAATACG GTTGCTAATC      60
TAATATGTGA ATCAGGTTTA AGAAAAGTTT TAGATTTCCA ACCTTGTTGA CTGGGAAAGA      120
GCAAAGTTTT TTGTAATCGA GTATCGTGTG TCTGTGCCAT TGTCGAAATA GTCATACTTA      180
TATCGTTCTG TTTATCTTAT CAATATGAAA ACTACATCGT TGATTGCCCT GACAATGCCT      240
TGGTCAATT                                         249

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(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

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AATTCTTGTC CCGGAGTCCA ACGTATATTT ACCCTCCTGC GAGCTAAAAG ACTATTATTC      60
TCCACTGCCA CAGTAGCCGC ATTCACCGCC GTATTCACAT CCCCTTTAAC CAATGCCACT      120

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GCGCTGCCTG CGATAATCTG CGAGTAGGCT ATGACTTTTT GCGTTCTTG GGGTGACAGT 180  
 TTGCCTACAT CGCGTCCGTC CAACAGGGTT TCTCCACCA TCTCGCCGAC TGCCGCGCCG 240  
 ATTGCGCCGT CCCGACATTT GCCTTTATTT GCTACCGCCG ATGCACAGCC TGCTACGGCA 300  
 TGGGCTATCT TGTGGGCAAT GTAGTCTTCG CTGAGATTAA ATT 343

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AATTCTTCAA ACATCGTTTC GATAATCGGG TCGGTGTACA CACTGATGCG GTCGCCCCGCA 60  
 CGGCTTTGAC CGGCTCGGAA AATATAGGCG GTGGCTTTGC CGTCGGCGAT GTCGACGCAC 120  
 CAACGCCAGA TGGCGTCTTC GGTATTCAAA CAATCACCCG CACAGCTTTC ACCTGCGCGG 180  
 AATT 184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TATGCTCAAT CTCATTTTCA AAATGCAAAA CTTTCTGAT TTTTCTACT TTTTGCTCAA 60  
 TATTAGGAAG GTTTTAGGCA ATTGAAAATT TTTTGGCGCA TTTTATGCG TCAAATTCG 120

TTAACAGACT ATTTTTGCAA AGGTCTCCGT CTGTAAAAGC AAGGATAGGG CATCTGCCCT 180

TTTGATTGTT TGATTAACGA TACAAGGAGT TTCAAATGA GAGTTTTATA GTGGATTAAC 240

AAAAACCAGT ACAGCGTTGC CTCGCCTTGC CGTACTATTT GTACTGTCTG CGGCTTCGTC 300

GCCTTGTCCT GATTTAAATT TAATCCACTA TATGTGTTCA TGAAATGACT TGGGTCGGAG 360

GCTCAGGTAA TGCGCAACAA AGTTCATATT ATTGCGAAAT TTGCGAATCT GCAGGGCTTA 420

ACGATACGGG AAATCCTGAT AAATCTTTAG GATTGCCAAA CAATACGTTC AGTAATCCGC 480

CTGGTTGGGG AGCTACAATC GGAGCTTTAG CAGGTAGCCG CATAGGTATG CCTGAATTTG 540

GTACGTTTGC GAGCCATGCC ATTGAAAATT TCGACTGGTC ATGGTATCGA CGTTATAGGG 600

AAATTGCCGA AACGATTGAA CGAGAATATT CAGGCGGTTT GCCTTAATAG TTGAGGAGGT 660

CATGATGTTT GCCAAACATT ATCAATTCAT CGCACTCGGC ATCATGCTGC TTCTTTATAT 720

GTTGATTCTC TATACGACCG ATTTTTCCAA TCTGACGTAT TGGATGCTGT TTTTATCTG 780

TTTTATTACA GGAAAAATAT TAGCTCGTTT GTTAGAGAAA AGCTTTAAAT AAAATAGCAG 840

CTAGTCGCAA AAGGTCGTCT GAAACCTTTT CAGGCGGCCT TTCTAAAATA CATCCAACTT 900

CCTAATCCCT ATTTTTCAAA AAGGAAATCT ATGCCCCATC TGCAAAACCT GTCTTTGGGC 960

TTAAAGAAAA AGCTGCCTGT TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT 1020

CTGGCGGCTG TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA 1080

TACTGTCCGA GACCTTTGCA AAATCCCCA AAATCCCCTA AATGTCTTGG TGGGAATTTT 1140

GGGGAATTTT GCAAAGGTCT CATTCTATAA CTGTAAATAC TTTTAAATTT ATGACAAAAT 1200

AGTAAATATT GCTAAAATAA TATTGATGTC ATGAAATTTT TTCCTGCTCC ATGTCTGTTG 1260

GTTATCCTGG CTGTCATACC CCTTAAAACC TTAGCTGCCG ATGAAAACGA TGCAGAACTT	1320
ATCCGTTCCA TGCAGCGTCA GCAGCACATA GATGCTGAAT TGTAACTGA TGCAAATGTC	1380
CGTTTCGAGC AACCATTGGA GAAGAACAAT TATGTCCTGA GTGAAGATGA AACACCGTGT	1440
ACTCGGGTAA ATTACATTAG TTTAGATGAT AAGACGGCGC GCAAATTTTC TTTCTTCCT	1500
TCTGTGCTCA TGAAAGAAAC AGCTTTTAAA ACTGGGATGT GTTTAGGTTC CAATAATTTG	1560
AGCAGGCTAC AAAAAGCCGC GCAACAGATA CTGATTGTGC GTGGCTACCT CACTTCCCAA	1620
GCTATTATCC AACCACAGAA TATGGATTCTG GGAATTCTGA AATTACGGGT ATCAGCAGGC	1680
GAAATAGGGG ATATCCGCTA TGAAGAAAA CGGGATGGGA AGTCTGCCGA GGGCAGTATT	1740
AGTGCATTCA ATAACAAATT TCCCTTATAT AGGAACAAAA TTCTCAATCT TCGCGATGTA	1800
GAGCAGGGCT TGGAAAACCT GCGTCGTTTG CCGAGTGTTA AAACAGATAT TCAGATTATA	1860
CCGTCCGAAG AAGAAGGCAA AAGCGATTTA CAGATCAAAT GGCAGCAGAA TAAACCCATA	1920
CGGTTTCAGTA TCGGTATAGA TGATGCGGGC GGCAAAACGA CCGGCAAATA TCAAGGAAAT	1980
GTCGCTTTAT CGTTCGATAA CCCTTTGGGC TTAAGCGATT TGTTTTATGT TTCATATGGA	2040
CGCGGTTTGG TGCACAAAAC GGACTTGACT GATGCCACCG GTACGGAAAC TGAAAGCGGA	2100
TCCAGAAGTT ACAGCGTGCA TTATTCCGTG CCCGTAAAAA AATGGCTGTT TTCTTTTAAT	2160
CACAATGGAC ATCGTTACCA CGAAGCAACC GAAGGCTATT CCGTCAATTA CGATTACAAC	2220
GGCAAACAAT ATCAGAGCAG CCTGGCCGCC GAGCGCATGC TTTGGCGTAA CAGGTTTCAT	2280
AAAACCTCAG TCGGAATGAA ATTATGGACA CGCCAAACCT ATAAATACAT CGACGATGCC	2340
GAAATCGAAG TGCAACGCCG CCGCTCTGCA GGCTGGGAAG CCGAATTGCG CCACCGTGCT	2400

TACCTCAACC GTTGGCAGCT TGACGGCAAG TTGTCTTACA AACGCGGGAC CGGCATGCGC	2460
CAAAGTATGC CCGCACCTGA AGAAAACGGC GGCGGTACTA TTCCAGGCAC ATCCCGTATG	2520
AAAATCATAA CCGCCGGATT GGATGCAGCG GCCCCGTTTA TGTTGGGCAA ACAGCAGTTT	2580
TTCTACGCAA CCGCCATTCA AGCTCAATGG AACAAAACGC CTTTGGTTGC CCAAGACAAG	2640
TTGTCTATCG GCAGCCGCTA CACCGTTCGC GGATTTGATG GGGAGCAGAG TCTTTTCGGA	2700
GAGCGAGGTT TCTACTGGCA GAATACTTTA ACTTGGTATT TTCATCCGAA CCATCAGTTC	2760
TATCTCGGTG CGGACTATGG CCGCGTATCT GGCGAAAGTG CACAATATGT ATCGGGCAAG	2820
CAGCTGATGG GTGCAGTGGT CGGCTTCAGA GGAGGGCATA AAGTAGGCGG TATGTTTGCT	2880
TATGATCTGT TTGCCGGCAA GCCGCTTCAT AAACCCAAAG GCTTTCAGAC GACCAACACC	2940
GTTTACGGCT TCAACTTGAA TTACAGTTTC TAACCTCTGA ATTTTTTTTAC TGATATTTAG	3000
ACGGTCTTTC CTTATCCTCA GACTGTCAAA CTTTACCTAC GTACTTGGCG CGCAGTACGT	3060
TCATCTTCAA AATGGAATAG ACATGAATAA AGGTTTACAT CGCATTATCT TTAGTAAAAA	3120
GCACAGCACC ATGGTTGCAG TAGCCGAAAC TGCCAACAGC CAGGGCAAAG GTAAACAGGC	3180
AGGCAGTTCG GTTTCTGTTT CACTGAAAAC TTCAGGCGAC CTTTGCGGCA AACTCAAAAC	3240
CACCCTTAAA ACCTTGGTCT GCTCTTTGGT TTCCCTGAGT ATGGTATTGC CTGCCCATGC	3300
CCAAATTACC ACCGACAAAT CAGCACCTAA AAACCAGCAG GTCGTTATCC TTAAAACCAA	3360
CACTGGTGCC CCCTTGGTGA ATATCCAAAC TCCGAATGGA CGCGGATTGA GCCACAACCG	3420
CTATACGCAG TTTGATGTTG ACAACAAAGG GGCAGTGTTA AACAAACGACC GTAACAATAA	3480
TCCGTTTCTG GTCAAAGGCA GTGCGCAATT GATTTTGAAC GAGGTACGCG GTACGGCTAG	3540

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CAAACCTCAAC	GGCATCGTTA	CCGTAGGCGG	TCAAAAGGCC	GACGTGATTA	TTGCCAACCC	3600
CAACGGCATT	ACCGTTAATG	GCGGCGGCTT	TAAAAATGTC	GGTCGGGGCA	TCTTAACTAT	3660
CGGTGCGCCC	CAAATCGGCA	AAGACGGTGC	ACTGACAGGA	TTTGATGTGC	GTCAAGGCAC	3720
ATTGACCGTA	GGAGCAGCAG	GTTGGAATGA	TAAAGGCGGA	GCCGACTACA	CCGGGGTACT	3780
TGCTCGTGCA	GTTGCTTTGC	AGGGGAAATT	ACAGGGTAAA	AACCTGGCGG	TTTCTACCGG	3840
TCCTCAGAAA	GTAGATTACG	CCAGCGGCGA	AATCAGTGCA	GGTACGGCAG	CGGGTACGAA	3900
ACCGACTATT	GCCCTTGATA	CTGCCGCACT	GGGCGGTATG	TACGCCGACA	GCATCACACT	3960
GATTGCCAAT	GAAAAAGGCG	TAGGCGTCAA	AAATGCCGGC	ACACTCGAAG	CGGCCAAGCA	4020
ATTGATTGTG	ACTTCGTCAG	GCCGCATTGA	AAACAGCGGC	CGCATCGCCA	CCACTGCCGA	4080
CGGCACCGAA	GCTTCACCGA	CTTATCTCTC	CATCGAAACC	ACCGAAAAAG	GAGCGGCAGG	4140
CACATTTATC	TCCAATGGTG	GTCGGATCGA	GAGCAAAGGC	TTATTGGTTA	TTGAGACGGG	4200
AGAAGATATC	AGCTTGCGTA	ACGGAGCCGT	GGTGCAGAAT	AACGGCAGTC	GCCCAGCTAC	4260
CACGGTATTA	AATGCTGGTC	ATAATTTGGT	GATTGAGAGT	AAAACATAATG	TGAACAATGC	4320
CAAAGGCTCG	GCTAATCTGT	CGGCCGGCGG	TCGTACTACG	ATCAATGATG	CTACTATTCA	4380
AGCGGGCAGT	TCCGTGTACA	GCTCCACCAA	AGGCGATACT	GAATTGGGTG	AAAATACCCG	4440
TATTATTGCT	GAAAACGTAA	CCGTATTATC	TAACGGTAGT	ATTGGCAGTG	CTGCTGTAAT	4500
TGAGGCTAAA	GACACTGCAC	ACATTGAATC	GGGCAAACCG	CTTCTTTAG	AAACCTCGAC	4560
CGTTGCCTCC	AACATCCGTT	TGAACAACGG	TAACATTAAA	GGCGGAAAGC	AGCTTGCTTT	4620
ACTGGCAGAC	GATAACATTA	CTGCCAAAAC	TACCAATCTG	AATACTCCCG	GCAATCTGTA	4680

TGTTCATACA	GGTAAAGATC	TGAATTTGAA	TGTTGATAAA	GATTTGTCTG	CCGCCAGCAT	4740
CCATTTGAAA	TCGGATAACG	CTGCCCATAT	TACCGGCACC	AGTAAAACCC	TCACTGCCTC	4800
AAAAGACATG	GGTGTGGAGG	CAGGCTTGCT	GAATGTTACC	AATACCAATC	TGCGTACCAA	4860
CTCGGGTAAT	CTGCACATTC	AGGCAGCCAA	AGGCAATATT	CAGCTTCGCA	ATACCAAGCT	4920
GAACGCAGCC	AAGGCTCTCG	AAACCACCGC	ATTGCAGGGC	AATATCGTTT	CAGACGGCCT	4980
TCATGCTGTT	TCTGCAGACG	GTCATGTATC	CTTATTGGCC	AACGGTAATG	CCGACTTTAC	5040
CGGTCACAAT	ACCCTGACAG	CCAAGGCCGA	TGTCAATGCA	GGATCGGTTG	GTAAAGGCCG	5100
TCTGAAAGCA	GACAATACCA	ATATCACTTC	ATCTTCAGGA	GATATTACGT	TGGTTGCCGG	5160
CAACGGTATT	CAGCTTGGTG	ACGGAAAACA	ACGCAATTCA	ATCAACGGAA	AACACATCAG	5220
CATCAAAAC	AACGGTGGTA	ATGCCGACTT	AAAAAACCTT	AACGTCCATG	CCAAAAGCGG	5280
GGCATTGAAC	ATTCATTCCG	ACCGGGCATT	GAGCATAGAA	AATACCAAGC	TGGAGTCTAC	5340
CCATAATACG	CATCTTAATG	CACAACACGA	GCGGGTAACG	CTCAACCAAG	TAGATGCCTA	5400
CGCACACCGT	CATCTAAGCA	TTACCGGCAG	CCAGATTTGG	CAAAACGACA	AACTGCCTTC	5460
TGCCAACAAG	CTGGTGGCTA	ACGGTGTATT	GGCACTCAAT	GCGCGCTATT	CCCAAATTGC	5520
CGACAACACC	ACGCTGAGAG	CGGGTGCAAT	CAACCTTACT	GCCGGTACCG	CCCTAGTCAA	5580
GCGCGGCAAC	ATCAATTGGA	GTACCGTTTC	GACCAAGACT	TTGGAAGATA	ATGCCGAATT	5640
AAAACCATTG	GCCGGACGGC	TGAATATTGA	AGCAGGTAGC	GGCACATTAA	CCATCGAACC	5700
TGCCAACCGC	ATCAGTGCGC	ATACCGACCT	GAGCATCAAA	ACAGGCGGAA	AATTGCTGTT	5760
GTCTGCAAAA	GGAGGAAATG	CAGGTGCGCC	TAGTGCTCAA	GTTTCCTCAT	TGGAAGCAAA	5820

AGGCAATATC	CGTCTGGTTA	CAGGAGAAAC	AGATTTAAGA	GGTTCTAAAA	TTACAGCCGG	5880
TAAAACTTG	GTTGTCGCCA	CCACCAAAGG	CAAGTTGAAT	ATCGAAGCCG	TAAACAACCTC	5940
ATTGAGCAAT	TATTTTCCTA	CACAAAAAGC	GGCTGAACTC	AACCAAAAAAT	CCAAAGAATT	6000
GGAACAGCAG	ATTGCGCAGT	TGAAAAAAG	CTCGCCTAAA	AGCAAGCTGA	TTCCAACCCT	6060
GCAAGAAGAA	CGCGACCGTC	TCGCTTTCTA	TATTCAAGCC	ATCAACAAGG	AAGTTAAAGG	6120
TAAAAACCC	AAAGGCAAAG	AATACCTGCA	AGCCAAGCTT	TCTGCACAAA	ATATTGACTT	6180
GATTTCCGCA	CAAGGCATCG	AAATCAGCGG	TTCCGATATT	ACCGCTTCCA	AAAAACTGAA	6240
CCTTCACGCC	GCAGGCGTAT	TGCCAAAGGC	AGCAGATTCA	GAGGCGGCTG	CTATTCTGAT	6300
TGACGGCATA	ACCGACCAAT	ATGAAATTGG	CAAGCCCACC	TACAAGAGTC	ACTACGACAA	6360
AGCTGCTCTG	AACAAGCCTT	CACGTTTGAC	CGGACGTACG	GGGGTAAGTA	TTCATGCAGC	6420
TGCGGCACTC	GATGATGCAC	GTATTATTAT	CGGTGCATCC	GAAATCAAAG	CTCCCTCAGG	6480
CAGCATAGAC	ATCAAAGCCC	ATAGTGATAT	TGTACTGGAG	GCTGGACAAA	ACGATGCCTA	6540
TACCTTCTTA	AAAACCAAAG	GTAAAAGCGG	CAAAATCATC	AGAAAAACCA	AGTTTACCAG	6600
CACCCGCGAC	CACCTGATTA	TGCCAGCCCC	CGTCGAGCTG	ACCGCCAACG	GTATCACGCT	6660
TCAGGCAGGC	GGCAACATCG	AAGCTAATAC	CACCCGCTTC	AATGCCCCCTG	CAGGTAAAGT	6720
TACCCTGGTT	GCGGGTGAAG	AGCTGCAACT	GCTGGCAGAA	GAAGGCATCC	ACAAGCACGA	6780
GTTGGATGTC	CAAAAAAGCC	GCCGCTTTAT	CGGCATCAAG	GTAGGTAAGA	GCAATTACAG	6840
TAAAAACGAA	CTGAACGAAA	CCAAATTGCC	TGTCCGCGTC	GTCGCCCAAA	CTGCAGCCAC	6900
CCGTTCAGGC	TGGGATACCG	TGCTCGAAGG	TACCGAATTC	AAAACCACGC	TGGCCGGTGC	6960

CGACATTCAG	GCAGGTGTAG	GCGAAAAAGC	CCGTGTCGAT	GCGAAAATTA	TCCTCAAAGG	7020
CATTGTGAAC	CGTATCCAGT	CGGAAGAAAA	ATTAGAAACC	AACTCAACCG	TATGGCAGAA	7080
ACAGGCCGGA	CGCGGCAGCA	CTATCGAAAC	GCTAAAACTG	CCCAGCTTCG	AAAGCCCTAC	7140
TCCGCCCAAA	TTGTCCGCAC	CCGGCGGCTA	TATCGTCGAC	ATTCCGAAAG	GCAATCTGAA	7200
AACCGAAATC	GAAAAGCTGT	CCAAACAGCC	CGAGTATGCC	TATCTGAAAC	AGCTCCAAGT	7260
AGCGAAAAAC	ATCAACTGGA	ATCAGGTGCA	GCTTGCTTAC	GACAGATGGG	ACTACAAACA	7320
GGAGGGCTTA	ACCGAAGCAG	GTGCGGCGAT	TATCGCACTG	GCCGTTACCG	TGGTCACCTC	7380
AGGCGCAGGA	ACCGGAGCCG	TATTGGGATT	AAACGGTGCG	GCCGCCGCCG	CAACCGATGC	7440
AGCATTCGCC	TCTTTGGCCA	GCCAGGCTTC	CGTATCGTTC	ATCAACAACA	AAGGCGATGT	7500
CGGCAAAACC	CTGAAAGAGC	TGGGCAGAAG	CAGCACGGTG	AAAAATCTGG	TGGTTGCCGC	7560
CGCTACCGCA	GGCGTAGCCG	ACAAAATCGG	CGCTTCGGCA	CTGAACAATG	TCAGCGATAA	7620
GCAGTGGATC	AACAACCTGA	CCGTCAACCT	AGCCAATGCG	GGCAGTGCCG	CACTGATTAA	7680
TACCGCTGTC	AACGGCGGCA	GCCTGAAAGA	CAATCTGGAA	GCGAATATCC	TTGCGGCTTT	7740
GGTCAATACC	GCGCATGGAG	AAGCAGCCAG	TAAAATCAAA	CAGTTGGATC	AGCACTACAT	7800
AGTCCACAAG	ATTGCCCATG	CCATAGCGGG	CTGTGCGGCA	GCGGCGGCGA	ATAAGGGCAA	7860
GTGTCAGGAT	GGTGCGATAG	GTGCGGCTGT	GGGCGAGATA	GTCGGGGAGG	CTTTGACAAA	7920
CGGCAAAAAT	CCTGACACTT	TGACAGCTAA	AGAACGCGAA	CAGATTTTGG	CATACAGCAA	7980
ACTGGTTGCC	GGTACGGTAA	GCGGTGTGGT	CGGCGGCGAT	GTAAATGCGG	CGGCGAATGC	8040
GGCTGAGGTA	GCGGTGAAAA	ATAATCAGCT	TAGCGACAAA	GAGGGTAGAG	AATTTGATAA	8100



CGAAATGACT GCATGCGCCA AACAGAATAA TCCTCAACTG TGCAGAAAAA ATACTGTAAA	8160
AAAGTATCAA AATGTTGCTG ATAAAAGACT TGCTGCTTCG ATTGCAATAT GTACGGATAT	8220
ATCCCGTAGT ACTGAATGTA GAACAATCAG AAAACAACAT TTGATCGATA GTAGAAGCCT	8280
TCATTCATCT TGGGAAGCAG GTCTAATTGG TAAAGATGAT GAATGGTATA AATTATTCAG	8340
CAAATCTTAC ACCCAAGCAG ATTTGGCTTT ACAGTCTTAT CATTTGAATA CTGCTGCTAA	8400
ATCTTGGCTT CAATCGGGCA ATACAAAGCC TTTATCCGAA TGGATGTCCG ACCAAGGTTA	8460
TACACTTATT TCAGGAGTTA ATCCTAGATT CATTCCAATA CCAAGAGGGT TTGTAAAACA	8520
AAATACACCT ATTACTAATG TCAAATACCC GGAAGGCATC AGTTTCGATA CAAACCTAAA	8580
AAGACATCTG GCAAATGCTG ATGGTTTTAG TCAAGAACAG GGCATTAAAG GAGCCCATAA	8640
CCGCACCAAT TTTATGGCAG AACTAAATTC ACGAGGAGGA CGCGTAAAAT CTGAAACCCA	8700
AACTGATATT GAAGGCATTA CCCGAATTAA ATATGAGATT CCTACACTAG ACAGGACAGG	8760
TAAACCTGAT GGTGGATTTA AGGAAATTC AAGTATAAAA ACTGTTTATA ATCCTAAAAA	8820
ATTTTCTGAT GATAAAATAC TTCAAATGGC TCAAATGCT GCTTCACAAG GATATTCAAA	8880
AGCCTCTAAA ATTGCTCAAA ATGAAAGAAC TAAATCAATA TCGGAAAGAA AAAATGTCAT	8940
TCAATTCTCA GAAACCTTTG ACGGAATCAA ATTTAGATCA TATTTTGATG TAAATACAGG	9000
AAGAATTACA AACATTCACC CAGAATAATT TAAAGGAAAA ATTATGAAAA ATAATATTTT	9060
TCTAACTTA AATAAAAAAT CTATAAATAA CAACCATTTT GTTATTTTGA TTTTTTTTGA	9120
AACAATTTAC CAATTTGAAA CTAAAGATAC GCTTTTAGAG TGTTTTAAAA ATATTACAAC	9180
TACCGGACAT TTTGGAGTAA TAGGTGCTCA ATATGAAAAA ATAGATGCTA CCAGATGGAT	9240

TGGAGATTAT GAAGAGGTAA ATGGATTGTA GTATATTGAT AAAGCTCCTT CTATTTATTT 9300  
 TTCAGTTGGA GATGATTTC A TCCTGAAGA ATTAATTATA CCTATTAATT TAGCATATCA 9360  
 TTACTTTAAT ATTGCAATAT CTGATTTCTT AATAGCTCAC CCTGAATATC AAAAAAAGTG 9420  
 TAAAGAAATA CAAAAAACAT ATTCTCAAAC AAAGTGTAGC CTGCATGAAA CCTAAAATCC 9480  
 ATGCGTAAGG TGTGTGCTTC AGCACGCACG CGTTCCATGA TTTACGGCTC AATGCCGTCT 9540  
 GAAAAGCTCA CAATTTTTC A GACGGCATT GTTATGCAAG TAAATATTCA GATTCCCTAT 9600  
 ATACTGCCCC GACGCGTGCG TGCTGAAGAC ACCCCCTACG CTTGCTGCAG AACTTTCGGG 9660  
 TAAACCGGT GTGAGCATT A GCGCACCGTA TGCCAATGAG AACAGTCGCA TCCTGCTCAG 9720  
 CACCACGGAT ATCAGTTCGG AAAACGGCAA AATCAAAATT CAATCTTACG GTGACCAATA 9780  
 TTACTATGCG AGACAGAGCG AACTCTATAC CTTTGAACGC CGCAGCTACA AACTGGCAA 9840  
 ATGGTACAAC CGCAAACACA TTACCGAAGT CAAAGAACAC AAAAACGCCA AGCCCGACGC 9900  
 AGTAAACCTC AGCGCATCCC AAGGCATCGA CATCAAATCT GGTGGCAGCA TCGACGCCTA 9960  
 CGCCACCGCA TTCGATGCCC CCAAAGGCAG CATTAAACATC GAAGCCGGGC GGAAATTGAC 10020  
 ACTCTATGCC GTAGAAGAGC TCAACTACGA CAACTAGAC AGCCAAAAAA GGCGCAGATT 10080  
 TCTCGGCATC AGCTACAGCA AAGCACACGA CACCACCACC CAAGTCATGA AAACCGCGCT 10140  
 GCCCTCAAGG GTAGTTGCAG AATCAGCCAA CCTCCAATCG GGCTGGGATA CCAAAGTGC A 10200  
 AGGCACACAG TTTGAAACCA CACTGGGTGG CGCAACCATA CGCGCAGGCG TAGGTGAGCA 10260  
 GGCACGGGCA GATGCCAAGA TTATCCTCGA AGGGATCAAA AGCAGCATCC ACACAGAAAC 10320  
 CGTGAGCAGC AGCAAATCTA CTCTATGGCA AAAACAGGCA GGACGGGGCA GTAACATCGA 10380

AACCTTGCAA TTGCCGAGTT TCACCGGTCC CGTTGCGCCC GTACTGTCCG CACCCGGCGG 10440  
TTACATTGTC GACATTCCGA AAGGCAATCT GAAAACCCAA ATCGAAACCC TCACCAAGCA 10500  
GCCCCGAGTAT GCTTATTTGA AACAACTTCA AGTTGCGAAA AACATCAACT GGAATCAGGT 10560  
GCAGCTTGCT TACGATAAAT GGGACTACAA ACAGGAGGGC ATGACACCCG CAGCAGCAGC 10620  
TGTCGTCGTT ATCGTCGTAA CCGTATTGAC CTACGGTGCA CTGTCCGCCC CGGCAGCCGC 10680  
CGGAACGGCG GCGCGGGCAG GCGCAGGAGC GGGAGGAGCC GCAGCAGGAA CGGCAGCCGG 10740  
AACTGGAGTA GCAGCAGGAA CGGCAGCCAC AACC GGAGTA GCAGCAGGCA CATCAGCTGC 10800  
AGCTATCACC ACAGCCGCAG GCAAAGCCGC ACTGGCCAGT CTCGCCAGCC AAGCCGCAGT 10860  
TTCCCTCATC AACAAACAAAG GAGACATAAA CCATACCCTG AAAGAACTGG GCAAAGCAG 10920  
CACCGTCAGA CAGGCCGCCA CCGCCGCCGT AACCGCAGGC GTACTGCAGG GCATAAGCGG 10980  
GCTGAACACC CAAGCAGCCG AAGCCGTCAG CAAACATTTT CACAGTCCCG CAGCAGGCAA 11040  
ACTGACCGCT AACCTGATCA ACAGCACCGC TGCCGCAAGT GTCCATACCG CCATCAACGG 11100  
CGGCAGCCTG AAAGACAACT TGGGCGATGC CGCACTGGGT GCGATAGTCA GTACCGTACA 11160  
CGGAGAAGTA GCGAGCAAAA TCAAATTTAA TCTCAGCGAA GACTACATTG CCCACAAGAT 11220  
AGCCCATGCC GTAGCAGGCT GTGCATCGGC GGTAGCAAAT AAAGGCAAAT GTCGGGACGG 11280  
CGCAATCGGC GCGGCAGTCG GCGAGATGGT GGGAGAAACC CTGTTGGACG GACGCGATGT 11340  
AGGCAAACCTG TCACCCCAAG AACGCCAAAA AGTCATAGCC TACTCGCAGA TTATCGCAGG 11400  
CAGCGCAGTG GCATTGGTTA AAGGGGATGT GAATACGGCG GTGAATGCGG CTACTGTGGC 11460  
AGTGGAGAAT AATAGTCTTT TAGCTCGCAG GAGGGTAAAT ATACGTTGGA CTCCGCGACA 11520

AGAATTGGAA CATGAATATG CCATTCTTGA AATCCAGGCC ATTACCAATC AAATCCGAAG 11580  
 GCTGGATCCG AAATTTAACG GGATTGCTAT TCTGAGGACT CCTGGAGAGC CGTGGACAAG 11640  
 ACATGATGTA CAAACATACA GGCAATATTA TAATCAATTA AGGGAATCCA GAGGCTTTGC 11700  
 TGTTGAACCA ATTTATAGAA TCAGGATAAA CAACGGCAAT GAATTTAACC GTATCATGTC 11760  
 ATCAAAATAC CCTTATAATG AGCTTTATGT AGCCAATCCT AAATCGGCGA CGGGGTATTT 11820  
 TAGGGTAGAT TCGTATGATC CTGCGACAAG GGAAATTATT TCAAGAAAAT TTACCCAATT 11880  
 TTCTCAAATC CAAGAAAGTA CGGGGATTGG TTATATCAAG GAGGCTGTTA GAAAATATAG 11940  
 CCCTGGTACT GTCATTTCCA ATGTTCCAAG TACACCTACT ACGATAAGAG GAAGAAAGCT 12000  
 TGAAGGAAAA CTTATTTTAG AAGTTCCTGC TCAGGTCAAT CCAATTCCAC AATCTGTATT 12060  
 AAGGGCGGCA CAAGAAGAAA ATGTTATCAT TAGAGATACA ACAGGAAGGA TTTACAAATG 12120  
 AAGAAAGATA TTTTTTATTG TGAGCAGTGG TCTTATGGTT ATAAGAGACT TCATAAGCCT 12180  
 TTTTCTGAGA AACAAGCTGA GGAAAAACAT CTTAAAGGGG AGTTATATAC TGCCGTAATA 12240  
 GGTTCGGCGA CACAACCTGA ATATGTAATT ACCTTGCGAG AGGAAGTAGG TTTTTTTTCG 12300  
 GTAAATTTTT TCGATAAATT TGGAAGGGAT TATTTAACCC ATCAATTTCA AAAATATTCC 12360  
 AATTCGAATT ATTATTTTCT TTCTATGGCT GTATGGAGAG ATTATATAAC TTTGGAATCT 12420  
 CATGACTTAG CAGAAGGATA TACTTATTTT TTCAATGAAA ATACGGATGA TTGCTATGTT 12480  
 TTGAAACAAG ATTTTATTAA TAATGAGCGA TATGAAAAAA CAGAATTATA TTCCCAAAAA 12540  
 GATAAGGTAA TTCTATTTCC AAAGTTTGGT GAATATGATT TGGTGTTAAA TCCGGACATT 12600  
 ATTTAATTAA GTTTTAAGGC CGTCTGAAAA AAATTTCAAA CGGCTTTTAT TATTGGGTTT 12660

REPLACEMENT SHEET (RULE 26)

ACTGACAAAC AATTGCTGAA AGCTATTGGC GAAGGAAGGG ACACGACAGG TAAAATGACC 13860  
 GAGCAGTTAT TTGACTCTTT AGCTAAACAA AATGGCTTCA GAGTGCTTTC GGGCGGCAAA 13920  
 TACGGCGGAA ATAACGGTTT TGATCATGTA TGGCAGGCTG CCGATGGTAG TGTCGTTTTG 13980  
 ATTGTAGAAA GTAAGCAGAT TAGGAACGGT ACGGTACAGC TGAATCCGAA TGGTGCGGGT 14040  
 GGATATACGC AAATGAGTGA GGATTGGATT AGACAAGTTT TAGATCAATT ACCCGATGGT 14100  
 AGTCCCGCTA AAGCTGCTGT CTTCAAAGCA AATAAGAACG GCACATTAAA AACAGCAATA 14160  
 GCAGGCGTTG ATCGTCAAAC AGGTAAGGCC GTTATTCTTC CTGTCAAAGT TCCTTCTAAA 14220  
 ACCAATATAA GGAGATAACA ATGGGGCACA ATATGATGAC CACCCAAAAA TGGTATGAGC 14280  
 ATATTACTAA TGTAATCATA GGCAATACTG CTAATTTCAA TAGCGGTTGC CTTGACTCTA 14340  
 TAGATTATGT AGATGAAAGA AAAGGCGTTC CGCTTGCAGC TATGCAACAT ATTTTCATGG 14400  
 ACGTTAGAGC TGCAGCTTCC CATGCCTATC TATTTGAACA TGATCTTAAG AAATTCAAGC 14460  
 AATATGCTTA TGTTGCAGGA AAGCTGGGGG TTTTGCTGAG TGTAATTCT ACAGACCCTG 14520  
 AACCCCTTCTT CTTTCCCTGT GACATGCTCA ACATTCAAAA TCCGATGTTT CTGATGCTGA 14580  
 TGAGCGACAG CCCACAGCTG CGTGAGTTTC TGGTGCGCAA TATCGACAAC ATCGCCAACG 14640  
 ATACAGAAGC CTTTATAAAC CGCTACGACC TCAACCGGCA TATGATTTAC AATACTCTGC 14700  
 TGATGGTGGA GGGTAAGCAG CTTGATCGGT TGAAACAACG TAGCGAGAAA GTCTTGCGCGC 14760  
 ATCCCACCCC TAGCAAATGG CTGCAAAAGC GGTTGTACGA TTACCGCTTC TTCCTCGCTT 14820  
 TCGCCGAACA GGATGCCGAG GCAATGAAAG CCGCCTTAGA GCCGCTTTTC GATAAAAAAA 14880  
 CCGCGCGTAT GGCTGCCAAA GAAACATTGT CCTATTTCTGA TTTCTACCTG CAGCCGCAAA 14940

TCGTTACCTA CGCCAAAATC GCATCCATGC ACGGTTTCGA TTTGGGCATA GATCAAGAAA 15000

TCTCACCGAG GGATTTGATT GTTTACGATC CGCTGCCGGC AGACGAATAT CAAGACATCT 15060

TCGATTTTAT GAAACAGTAT GACTTGTCTT ACCCGTATGA ATATCTGCAG GATTGGATAG 15120

ATTACTATAC GTTCAAAACC GATAAGCTGG TATTTGGTAA CGCGAAGCGA GAGTGAGCCG 15180

TAAAACTCTG AGCTCCTGTT TTATAGATTA CAACTTTAGG CCGTCTTAAA GCTGAAAGAT 15240

TTTCGAAAGC TATAAATTGA AGCCCTTCCA CAGTACATAG ATCTGTGTTG TGGCGGGGCT 15300

TTACCACGCT GATTGCCGGA GAAGAACTCA ACCTGCTGGC AAAACAAGGC ATGAGATCTT 15360

TGCAATAACA TGAGTTGAGA CCTTTGCAAA AAAGCCCTTC CCCGACATCC GAAACCCAAA 15420

CACAGGATTT CGGCTGTTTT CGTACCAAAT ACCTCCTAAT TTTACCCAAA TACCCCTTA 15480

ATCCTCCTCG GACACCCGAT AATCAGGCAT CCGGGCTGCC TTTTAGGCGG CAGCGGGCGC 15540

ATTTAGCCTG TTGGCCGCTT TCAACAGGTT CAAACACATC GCCTTCAGGT GGCTTTGCGC 15600

ACTCACTTTG TCATTTCCAA 15620

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Met Lys Phe Phe Pro Ala Pro Cys Leu Leu Val Ile Leu Ala Val Ile  
 1 5 10 15

Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg  
 20 25 30

Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala  
 35 40 45

Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser  
 50 55 60

Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp  
 65 70 75 80

Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu  
 85 90 95

Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg  
 100 105 110

Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr  
 115 120 125

Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys  
 130 135 140

Leu Arg Val Ser Ala Gly Glu Ile Gly Asp Ile Arg Tyr Glu Glu Lys  
 145 150 155 160

Arg Asp Gly Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys  
 165 170 175

Phe Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln  
 180 185 190

09928457.031401



Gly	Leu	Glu	Asn	Leu	Arg	Arg	Leu	Pro	Ser	Val	Lys	Thr	Asp	Ile	Gln	195	200	205	
Ile	Ile	Pro	Ser	Glu	Glu	Glu	Gly	Lys	Ser	Asp	Leu	Gln	Ile	Lys	Trp	210	215	220	
Gln	Gln	Asn	Lys	Pro	Ile	Arg	Phe	Ser	Ile	Gly	Ile	Asp	Asp	Ala	Gly	225	230	235	240
Gly	Lys	Thr	Thr	Gly	Lys	Tyr	Gln	Gly	Asn	Val	Ala	Leu	Ser	Phe	Asp	245	250	255	
Asn	Pro	Leu	Gly	Leu	Ser	Asp	Leu	Phe	Tyr	Val	Ser	Tyr	Gly	Arg	Gly	260	265	270	
Leu	Val	His	Lys	Thr	Asp	Leu	Thr	Asp	Ala	Thr	Gly	Thr	Glu	Thr	Glu	275	280	285	
Ser	Gly	Ser	Arg	Ser	Tyr	Ser	Val	His	Tyr	Ser	Val	Pro	Val	Lys	Lys	290	295	300	
Trp	Leu	Phe	Ser	Phe	Asn	His	Asn	Gly	His	Arg	Tyr	His	Glu	Ala	Thr	305	310	315	320
Glu	Gly	Tyr	Ser	Val	Asn	Tyr	Asp	Tyr	Asn	Gly	Lys	Gln	Tyr	Gln	Ser	325	330	335	
Ser	Leu	Ala	Ala	Glu	Arg	Met	Leu	Trp	Arg	Asn	Arg	Phe	His	Lys	Thr	340	345	350	
Ser	Val	Gly	Met	Lys	Leu	Trp	Thr	Arg	Gln	Thr	Tyr	Lys	Tyr	Ile	Asp	355	360	365	
Asp	Ala	Glu	Ile	Glu	Val	Gln	Arg	Arg	Arg	Ser	Ala	Gly	Trp	Glu	Ala	370	375	380	
Glu	Leu	Arg	His	Arg	Ala	Tyr	Leu	Asn	Arg	Trp	Gln	Leu	Asp	Gly	Lys	385	390	395	400

Leu Ser Tyr Lys Arg Gly Thr Gly Met Arg Gln Ser Met Pro Ala Pro  
 405 410 415

Glu Glu Asn Gly Gly Gly Thr Ile Pro Gly Thr Ser Arg Met Lys Ile  
 420 425 430

Ile Thr Ala Gly Leu Asp Ala Ala Ala Pro Phe Met Leu Gly Lys Gln  
 435 440 445

Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro  
 450 455 460

Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg  
 465 470 475 480

Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp  
 485 490 495

Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu  
 500 505 510

Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser  
 515 520 525

Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys  
 530 535 540

Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His  
 545 550 555 560

Lys Pro Lys Gly Phe Gln Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu  
 565 570 575

Asn Tyr Ser Phe  
 580

(2) INFORMATION FOR SEQ ID NO: 38:

REPLACEMENT SHEET (RULE 26)

00020457-001404

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..1981

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Asn Lys Gly Leu His Arg Ile Ile Phe Ser Lys Lys His Ser Thr  
 1                                5                                10                                15

Met Val Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln  
                               20                                25                                30

Ala Gly Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Leu Cys  
                               35                                40                                45

Gly Lys Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser  
                               50                                55                                60

Leu Ser Met Val Leu Pro Ala His Ala Gln Ile Thr Thr Asp Lys Ser  
 65                                70                                75                                80

Ala Pro Lys Asn Gln Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala  
                               85                                90                                95

Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn  
                               100                                105                                110

"09023457" DB1401

Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn			
115	120	125	
Asp Arg Asn Asn Asn Pro Phe Leu Val Lys Gly Ser Ala Gln Leu Ile			
130	135	140	
Leu Asn Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr			
145	150	155	160
Val Gly Gly Gln Lys Ala Asp Val Ile Ile Ala Asn Pro Asn Gly Ile			
	165	170	175
Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr			
	180	185	190
Ile Gly Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp			
	195	200	205
Val Arg Gln Gly Thr Leu Thr Val Gly Ala Ala Gly Trp Asn Asp Lys			
	210	215	220
Gly Gly Ala Asp Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln			
225	230	235	240
Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys			
	245	250	255
Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr			
	260	265	270
Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala			
	275	280	285
Asp Ser Ile Thr Leu Ile Ala Asn Glu Lys Gly Val Gly Val Lys Asn			
	290	295	300
Ala Gly Thr Leu Glu Ala Ala Lys Gln Leu Ile Val Thr Ser Ser Gly			
305	310	315	320

Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu  
325 330 335

Ala Ser Pro Thr Tyr Leu Ser Ile Glu Thr Thr Glu Lys Gly Ala Ala  
340 345 350

Gly Thr Phe Ile Ser Asn Gly Gly Arg Ile Glu Ser Lys Gly Leu Leu  
355 360 365

Val Ile Glu Thr Gly Glu Asp Ile Ser Leu Arg Asn Gly Ala Val Val  
370 375 380

Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala Gly His  
385 390 395 400

Asn Leu Val Ile Glu Ser Lys Thr Asn Val Asn Asn Ala Lys Gly Ser  
405 410 415

Ala Asn Leu Ser Ala Gly Gly Arg Thr Thr Ile Asn Asp Ala Thr Ile  
420 425 430

Gln Ala Gly Ser Ser Val Tyr Ser Ser Thr Lys Gly Asp Thr Glu Leu  
435 440 445

Gly Glu Asn Thr Arg Ile Ile Ala Glu Asn Val Thr Val Leu Ser Asn  
450 455 460

Gly Ser Ile Gly Ser Ala Ala Val Ile Glu Ala Lys Asp Thr Ala His  
465 470 475 480

Ile Glu Ser Gly Lys Pro Leu Ser Leu Glu Thr Ser Thr Val Ala Ser  
485 490 495

Asn Ile Arg Leu Asn Asn Gly Asn Ile Lys Gly Gly Lys Gln Leu Ala  
500 505 510

009228457 081401

Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu Asn Thr  
 515 520 525

Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val  
 530 535 540

Asp Lys Asp Leu Ser Ala Ala Ser Ile His Leu Lys Ser Asp Asn Ala  
 545 550 555 560

Ala His Ile Thr Gly Thr Ser Lys Thr Leu Thr Ala Ser Lys Asp Met  
 565 570 575

Gly Val Glu Ala Gly Leu Leu Asn Val Thr Asn Thr Asn Leu Arg Thr  
 580 585 590

Asn Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile Gln Leu  
 595 600 605

Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr Ala Leu  
 610 615 620

Gln Gly Asn Ile Val Ser Asp Gly Leu His Ala Val Ser Ala Asp Gly  
 625 630 635 640

His Val Ser Leu Leu Ala Asn Gly Asn Ala Asp Phe Thr Gly His Asn  
 645 650 655

Thr Leu Thr Ala Lys Ala Asp Val Asn Ala Gly Ser Val Gly Lys Gly  
 660 665 670

Arg Leu Lys Ala Asp Asn Thr Asn Ile Thr Ser Ser Ser Gly Asp Ile  
 675 680 685

Thr Leu Val Ala Gly Asn Gly Ile Gln Leu Gly Asp Gly Lys Gln Arg  
 690 695 700

Asn Ser Ile Asn Gly Lys His Ile Ser Ile Lys Asn Asn Gly Gly Asn  
 705 710 715 720

Ala Asp Leu Lys Asn Leu Asn Val His Ala Lys Ser Gly Ala Leu Asn  
725 730 735

Ile His Ser Asp Arg Ala Leu Ser Ile Glu Asn Thr Lys Leu Glu Ser  
740 745 750

Thr His Asn Thr His Leu Asn Ala Gln His Glu Arg Val Thr Leu Asn  
755 760 765

Gln Val Asp Ala Tyr Ala His Arg His Leu Ser Ile Thr Gly Ser Gln  
770 775 780

Ile Trp Gln Asn Asp Lys Leu Pro Ser Ala Asn Lys Leu Val Ala Asn  
785 790 795 800

Gly Val Leu Ala Leu Asn Ala Arg Tyr Ser Gln Ile Ala Asp Asn Thr  
805 810 815

Thr Leu Arg Ala Gly Ala Ile Asn Leu Thr Ala Gly Thr Ala Leu Val  
820 825 830

Lys Arg Gly Asn Ile Asn Trp Ser Thr Val Ser Thr Lys Thr Leu Glu  
835 840 845

Asp Asn Ala Glu Leu Lys Pro Leu Ala Gly Arg Leu Asn Ile Glu Ala  
850 855 860

Gly Ser Gly Thr Leu Thr Ile Glu Pro Ala Asn Arg Ile Ser Ala His  
865 870 875 880

Thr Asp Leu Ser Ile Lys Thr Gly Gly Lys Leu Leu Leu Ser Ala Lys  
885 890 895

Gly Gly Asn Ala Gly Ala Pro Ser Ala Gln Val Ser Ser Leu Glu Ala  
900 905 910

09223457-001401

Lys Gly Asn Ile Arg Leu Val Thr Gly Glu Thr Asp Leu Arg Gly Ser

915

920

925

Lys Ile Thr Ala Gly Lys Asn Leu Val Val Ala Thr Thr Lys Gly Lys

930

935

940

Leu Asn Ile Glu Ala Val Asn Asn Ser Phe Ser Asn Tyr Phe Pro Thr

945

950

955

960

Gln Lys Ala Ala Glu Leu Asn Gln Lys Ser Lys Glu Leu Glu Gln Gln

965

970

975

Ile Ala Gln Leu Lys Lys Ser Ser Pro Lys Ser Lys Leu Ile Pro Thr

980

985

990

Leu Gln Glu Glu Arg Asp Arg Leu Ala Phe Tyr Ile Gln Ala Ile Asn

995

1000

1005

Lys Glu Val Lys Gly Lys Lys Pro Lys Gly Lys Glu Tyr Leu Gln Ala

1010

1015

1020

Lys Leu Ser Ala Gln Asn Ile Asp Leu Ile Ser Ala Gln Gly Ile Glu

1025

1030

1035

1040

Ile Ser Gly Ser Asp Ile Thr Ala Ser Lys Lys Leu Asn Leu His Ala

1045

1050

1055

Ala Gly Val Leu Pro Lys Ala Ala Asp Ser Glu Ala Ala Ala Ile Leu

1060

1065

1070

Ile Asp Gly Ile Thr Asp Gln Tyr Glu Ile Gly Lys Pro Thr Tyr Lys

1075

1080

1085

Ser His Tyr Asp Lys Ala Ala Leu Asn Lys Pro Ser Arg Leu Thr Gly

1090

1095

1100

Arg Thr Gly Val Ser Ile His Ala Ala Ala Ala Leu Asp Asp Ala Arg

1105

1110

1115

1120



Ile Ile Ile Gly Ala Ser Glu Ile Lys Ala Pro Ser Gly Ser Ile Asp  
 1125 1130 1135

Ile Lys Ala His Ser Asp Ile Val Leu Glu Ala Gly Gln Asn Asp Ala  
 1140 1145 1150

Tyr Thr Phe Leu Lys Thr Lys Gly Lys Ser Gly Lys Ile Ile Arg Lys  
 1155 1160 1165

Thr Lys Phe Thr Ser Thr Arg Asp His Leu Ile Met Pro Ala Pro Val  
 1170 1175 1180

Glu Leu Thr Ala Asn Gly Ile Thr Leu Gln Ala Gly Gly Asn Ile Glu  
 1185 1190 1195 1200

Ala Asn Thr Thr Arg Phe Asn Ala Pro Ala Gly Lys Val Thr Leu Val  
 1205 1210 1215

Ala Gly Glu Glu Leu Gln Leu Leu Ala Glu Glu Gly Ile His Lys His  
 1220 1225 1230

Glu Leu Asp Val Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly  
 1235 1240 1245

Lys Ser Asn Tyr Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val  
 1250 1255 1260

Arg Val Val Ala Gln Thr Ala Ala Thr Arg Ser Gly Trp Asp Thr Val  
 1265 1270 1275 1280

Leu Glu Gly Thr Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln  
 1285 1290 1295

Ala Gly Val Gly Glu Lys Ala Arg Val Asp Ala Lys Ile Ile Leu Lys  
 1300 1305 1310

Gly Ile Val Asn Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser  
 1315 1320 1325

Thr Val Trp Gln Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu  
 1330 1335 1340

Lys Leu Pro Ser Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro  
 1345 1350 1355 1360

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile  
 1365 1370 1375

Glu Lys Leu Ser Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln  
 1380 1385 1390

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg  
 1395 1400 1405

Trp Asp Tyr Lys Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile  
 1410 1415 1420

Ala Leu Ala Val Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val  
 1425 1430 1435 1440

Leu Gly Leu Asn Gly Ala Ala Ala Ala Ala Thr Asp Ala Ala Phe Ala  
 1445 1450 1455

Ser Leu Ala Ser Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asp  
 1460 1465 1470

Val Gly Lys Thr Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn  
 1475 1480 1485

Leu Val Val Ala Ala Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala  
 1490 1495 1500

Ser Ala Leu Asn Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr  
 1505 1510 1515 1520

Val Asn Leu Ala Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val  
 1525 1530 1535

Asn Gly Gly Ser Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala  
 1540 1545 1550

Leu Val Asn Thr Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu  
 1555 1560 1565

Asp Gln His Tyr Ile Val His Lys Ile Ala His Ala Ile Ala Gly Cys  
 1570 1575 1580

Ala Ala Ala Ala Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly  
 1585 1590 1595 1600

Ala Ala Val Gly Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn  
 1605 1610 1615

Pro Asp Thr Leu Thr Ala Lys Glu Arg Glu Gln Ile Leu Ala Tyr Ser  
 1620 1625 1630

Lys Leu Val Ala Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn  
 1635 1640 1645

Ala Ala Ala Asn Ala Ala Glu Val Ala Val Lys Asn Asn Gln Leu Ser  
 1650 1655 1660

Asp Lys Glu Gly Arg Glu Phe Asp Asn Glu Met Thr Ala Cys Ala Lys  
 1665 1670 1675 1680

Gln Asn Asn Pro Gln Leu Cys Arg Lys Asn Thr Val Lys Lys Tyr Gln  
 1685 1690 1695

Asn Val Ala Asp Lys Arg Leu Ala Ala Ser Ile Ala Ile Cys Thr Asp  
 1700 1705 1710

Ile Ser Arg Ser Thr Glu Cys Arg Thr Ile Arg Lys Gln His Leu Ile  
 1715 1720 1725

Asp Ser Arg Ser Leu His Ser Ser Trp Glu Ala Gly Leu Ile Gly Lys  
 1730 1735 1740

Asp Asp Glu Trp Tyr Lys Leu Phe Ser Lys Ser Tyr Thr Gln Ala Asp  
 1745 1750 1755 1760

Leu Ala Leu Gln Ser Tyr His Leu Asn Thr Ala Ala Lys Ser Trp Leu  
 1765 1770 1775

Gln Ser Gly Asn Thr Lys Pro Leu Ser Glu Trp Met Ser Asp Gln Gly  
 1780 1785 1790

Tyr Thr Leu Ile Ser Gly Val Asn Pro Arg Phe Ile Pro Ile Pro Arg  
 1795 1800 1805

Gly Phe Val Lys Gln Asn Thr Pro Ile Thr Asn Val Lys Tyr Pro Glu  
 1810 1815 1820

Gly Ile Ser Phe Asp Thr Asn Leu Lys Arg His Leu Ala Asn Ala Asp  
 1825 1830 1835 1840

Gly Phe Ser Gln Glu Gln Gly Ile Lys Gly Ala His Asn Arg Thr Asn  
 1845 1850 1855

Phe Met Ala Glu Leu Asn Ser Arg Gly Gly Arg Val Lys Ser Glu Thr  
 1860 1865 1870

Gln Thr Asp Ile Glu Gly Ile Thr Arg Ile Lys Tyr Glu Ile Pro Thr  
 1875 1880 1885

Leu Asp Arg Thr Gly Lys Pro Asp Gly Gly Phe Lys Glu Ile Ser Ser  
 1890 1895 1900

Ile Lys Thr Val Tyr Asn Pro Lys Lys Phe Ser Asp Asp Lys Ile Leu  
 1905 1910 1915 1920

REPLACEMENT SHEET (RULE 26)

Thr Lys Asp Thr Leu Leu Glu Cys Phe Lys Asn Ile Thr Thr Thr Gly  
 35 40 45

His Phe Gly Val Ile Gly Ala Gln Tyr Glu Lys Ile Asp Ala Thr Arg  
 50 55 60

Trp Ile Gly Asp Tyr Glu Glu Val Asn Gly Phe Glu Tyr Ile Asp Lys  
 65 70 75 80

Ala Pro Ser Ile Tyr Phe Ser Val Gly Asp Asp Phe Asn Pro Glu Glu  
 85 90 95

Leu Ile Ile Pro Ile Asn Leu Ala Tyr His Tyr Phe Asn Ile Ala Ile  
 100 105 110

Ser Asp Phe Leu Ile Ala His Pro Glu Tyr Gln Lys Lys Cys Lys Glu  
 115 120 125

Ile Gln Lys Thr Tyr Ser Gln Thr Asn Cys Ser Leu His Glu Thr  
 130 135 140

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Val Leu Lys Thr Pro Pro Thr Leu Ala Ala Glu Leu Ser Gly Lys Thr  
 1 5 10 15  
 Gly Val Ser Ile Ser Ala Pro Tyr Ala Asn Glu Asn Ser Arg Ile Leu  
 20 25 30  
 Leu Ser Thr Thr Asp Ile Ser Ser Glu Asn Gly Lys Ile Lys Ile Gln  
 35 40 45  
 Ser Tyr Gly Asp Gln Tyr Tyr Tyr Ala Arg Gln Ser Glu Leu Tyr Thr  
 50 55 60  
 Phe Glu Arg Arg Ser Tyr Lys Thr Gly Lys Trp Tyr Asn Arg Lys His  
 65 70 75 80  
 Ile Thr Glu Val Lys Glu His Lys Asn Ala Lys Pro Asp Ala Val Asn  
 85 90 95  
 Leu Ser Ala Ser Gln Gly Ile Asp Ile Lys Ser Gly Gly Ser Ile Asp  
 100 105 110  
 Ala Tyr Ala Thr Ala Phe Asp Ala Pro Lys Gly Ser Ile Asn Ile Glu  
 115 120 125  
 Ala Gly Arg Lys Leu Thr Leu Tyr Ala Val Glu Glu Leu Asn Tyr Asp  
 130 135 140  
 Lys Leu Asp Ser Gln Lys Arg Arg Arg Phe Leu Gly Ile Ser Tyr Ser  
 145 150 155 160  
 Lys Ala His Asp Thr Thr Thr Gln Val Met Lys Thr Ala Leu Pro Ser  
 165 170 175  
 Arg Val Val Ala Glu Ser Ala Asn Leu Gln Ser Gly Trp Asp Thr Lys  
 180 185 190

Leu Gln Gly Thr Gln Phe Glu Thr Thr Leu Gly Gly Ala Thr Ile Arg  
 195 200 205

Ala Gly Val Gly Glu Gln Ala Arg Ala Asp Ala Lys Ile Ile Leu Glu  
 210 215 220

Gly Ile Lys Ser Ser Ile His Thr Glu Thr Val Ser Ser Ser Lys Ser  
 225 230 235 240

Thr Leu Trp Gln Lys Gln Ala Gly Arg Gly Ser Asn Ile Glu Thr Leu  
 245 250 255

Gln Leu Pro Ser Phe Thr Gly Pro Val Ala Pro Val Leu Ser Ala Pro  
 260 265 270

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Gln Ile  
 275 280 285

Glu Thr Leu Thr Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln  
 290 295 300

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys  
 305 310 315 320

Trp Asp Tyr Lys Gln Glu Gly Met Thr Pro Ala Ala Ala Ala Val Val  
 325 330 335

Val Ile Val Val Thr Val Leu Thr Tyr Gly Ala Leu Ser Ala Pro Ala  
 340 345 350

Ala Ala Gly Thr Ala Gly Ala Ala Gly Ala Gly Ala Gly Ala Ala  
 355 360 365

Ala Gly Thr Ala Ala Gly Thr Gly Val Ala Ala Gly Thr Ala Ala Thr  
 370 375 380

Thr Gly Val Ala Ala Gly Thr Ser Ala Ala Ala Ile Thr Thr Ala Ala  
 385 390 395 400



Gly Lys Ala Ala Leu Ala Ser Leu Ala Ser Gln Ala Ala Val Ser Leu  
 405 410 415

Ile Asn Asn Lys Gly Asp Ile Asn His Thr Leu Lys Glu Leu Gly Lys  
 420 425 430

Ser Ser Thr Val Arg Gln Ala Ala Thr Ala Ala Val Thr Ala Gly Val  
 435 440 445

Leu Gln Gly Ile Ser Gly Leu Asn Thr Gln Ala Ala Glu Ala Val Ser  
 450 455 460

Lys His Phe His Ser Pro Ala Ala Gly Lys Leu Thr Ala Asn Leu Ile  
 465 470 475 480

Asn Ser Thr Ala Ala Ala Ser Val His Thr Ala Ile Asn Gly Gly Ser  
 485 490 495

Leu Lys Asp Asn Leu Gly Asp Ala Ala Leu Gly Ala Ile Val Ser Thr  
 500 505 510

Val His Gly Glu Val Ala Ser Lys Ile Lys Phe Asn Leu Ser Glu Asp  
 515 520 525

Tyr Ile Ala His Lys Ile Ala His Ala Val Ala Gly Cys Ala Ser Ala  
 530 535 540

Val Ala Asn Lys Gly Lys Cys Arg Asp Gly Ala Ile Gly Ala Ala Val  
 545 550 555 560

Gly Glu Met Val Gly Glu Thr Leu Leu Asp Gly Arg Asp Val Gly Lys  
 565 570 575

Leu Ser Pro Gln Glu Arg Gln Lys Val Ile Ala Tyr Ser Gln Ile Ile  
 580 585 590

Ala Gly Ser Ala Val Ala Leu Val Lys Gly Asp Val Asn Thr Ala Val  
595 600 605

Asn Ala Ala Thr Val Ala Val Glu Asn Asn Ser Leu Leu Ala Arg Arg  
610 615 620

Arg Val Asn Ile Arg Trp Thr Pro Arg Gln Glu Leu Glu His Glu Tyr  
625 630 635 640

Ala Ile Leu Glu Ile Gln Ala Ile Thr Asn Gln Ile Arg Arg Leu Asp  
645 650 655

Pro Lys Phe Asn Gly Ile Ala Ile Leu Arg Thr Pro Gly Glu Pro Trp  
660 665 670

Thr Arg His Asp Val Gln Thr Tyr Arg Gln Tyr Tyr Asn Gln Leu Arg  
675 680 685

Glu Ser Arg Gly Phe Ala Val Glu Pro Ile Tyr Arg Ile Arg Ile Asn  
690 695 700

Asn Gly Asn Glu Phe Asn Arg Ile Met Ser Ser Lys Tyr Pro Tyr Asn  
705 710 715 720

Glu Leu Tyr Val Ala Asn Pro Lys Ser Ala Thr Gly Tyr Phe Arg Val  
725 730 735

Asp Ser Tyr Asp Pro Ala Thr Arg Glu Ile Ile Ser Arg Lys Phe Thr  
740 745 750

Gln Phe Ser Gln Ile Gln Glu Ser Thr Gly Ile Gly Tyr Ile Lys Glu  
755 760 765

Ala Val Arg Lys Tyr Ser Pro Gly Thr Val Ile Ser Asn Val Pro Ser  
770 775 780

Thr Pro Thr Thr Ile Arg Gly Arg Lys Leu Glu Gly Lys Leu Ile Leu  
785 790 795 800

Glu Val Pro Ala Gln Val Asn Pro Ile Pro Gln Ser Val Leu Arg Ala  
 805 810 815

Ala Gln Glu Glu Asn Val Ile Ile Arg Asp Thr Thr Gly Arg Ile Tyr  
 820 825 830

Lys

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 833 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Val Leu Lys Thr Pro Pro Thr Leu Ala Ala Glu Leu Ser Gly Lys Thr  
 1 5 10 15

Gly Val Ser Ile Ser Ala Pro Tyr Ala Asn Glu Asn Ser Arg Ile Leu  
 20 25 30

Leu Ser Thr Thr Asp Ile Ser Ser Glu Asn Gly Lys Ile Lys Ile Gln  
 35 40 45

Ser Tyr Gly Asp Gln Tyr Tyr Tyr Ala Arg Gln Ser Glu Leu Tyr Thr  
 50 55 60

Phe Glu Arg Arg Ser Tyr Lys Thr Gly Lys Trp Tyr Asn Arg Lys His  
 65 70 75 80

Ile Thr Glu Val Lys Glu His Lys Asn Ala Lys Pro Asp Ala Val Asn  
 85 90 95

Leu Ser Ala Ser Gln Gly Ile Asp Ile Lys Ser Gly Gly Ser Ile Asp  
100 105 110

Ala Tyr Ala Thr Ala Phe Asp Ala Pro Lys Gly Ser Ile Asn Ile Glu  
115 120 125

Ala Gly Arg Lys Leu Thr Leu Tyr Ala Val Glu Glu Leu Asn Tyr Asp  
130 135 140

Lys Leu Asp Ser Gln Lys Arg Arg Arg Phe Leu Gly Ile Ser Tyr Ser  
145 150 155 160

Lys Ala His Asp Thr Thr Thr Gln Val Met Lys Thr Ala Leu Pro Ser  
165 170 175

Arg Val Val Ala Glu Ser Ala Asn Leu Gln Ser Gly Trp Asp Thr Lys  
180 185 190

Leu Gln Gly Thr Gln Phe Glu Thr Thr Leu Gly Gly Ala Thr Ile Arg  
195 200 205

Ala Gly Val Gly Glu Gln Ala Arg Ala Asp Ala Lys Ile Ile Leu Glu  
210 215 220

Gly Ile Lys Ser Ser Ile His Thr Glu Thr Val Ser Ser Ser Lys Ser  
225 230 235 240

Thr Leu Trp Gln Lys Gln Ala Gly Arg Gly Ser Asn Ile Glu Thr Leu  
245 250 255

Gln Leu Pro Ser Phe Thr Gly Pro Val Ala Pro Val Leu Ser Ala Pro  
260 265 270

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Gln Ile  
275 280 285

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Glu Thr Leu Thr Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln  
 290 295 300

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys  
 305 310 315 320

Trp Asp Tyr Lys Gln Glu Gly Met Thr Pro Ala Ala Ala Val Val  
 325 330 335

Val Ile Val Val Thr Val Leu Thr Tyr Gly Ala Leu Ser Ala Pro Ala  
 340 345 350

Ala Ala Gly Thr Ala Gly Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala  
 355 360 365

Ala Gly Thr Ala Ala Gly Thr Gly Val Ala Ala Gly Thr Ala Ala Thr  
 370 375 380

Thr Gly Val Ala Ala Gly Thr Ser Ala Ala Ala Ile Thr Thr Ala Ala  
 385 390 395 400

Gly Lys Ala Ala Leu Ala Ser Leu Ala Ser Gln Ala Ala Val Ser Leu  
 405 410 415

Ile Asn Asn Lys Gly Asp Ile Asn His Thr Leu Lys Glu Leu Gly Lys  
 420 425 430

Ser Ser Thr Val Arg Gln Ala Ala Thr Ala Ala Val Thr Ala Gly Val  
 435 440 445

Leu Gln Gly Ile Ser Gly Leu Asn Thr Gln Ala Ala Glu Ala Val Ser  
 450 455 460

Lys His Phe His Ser Pro Ala Ala Gly Lys Leu Thr Ala Asn Leu Ile  
 465 470 475 480

Asn Ser Thr Ala Ala Ala Ser Val His Thr Ala Ile Asn Gly Gly Ser  
 485 490 495

Leu Lys Asp Asn Leu Gly Asp Ala Ala Leu Gly Ala Ile Val Ser Thr  
 500 505 510

Val His Gly Glu Val Ala Ser Lys Ile Lys Phe Asn Leu Ser Glu Asp  
 515 520 525

Tyr Ile Ala His Lys Ile Ala His Ala Val Ala Gly Cys Ala Ser Ala  
 530 535 540

Val Ala Asn Lys Gly Lys Cys Arg Asp Gly Ala Ile Gly Ala Ala Val  
 545 550 555 560

Gly Glu Met Val Gly Glu Thr Leu Leu Asp Gly Arg Asp Val Gly Lys  
 565 570 575

Leu Ser Pro Gln Glu Arg Gln Lys Val Ile Ala Tyr Ser Gln Ile Ile  
 580 585 590

Ala Gly Ser Ala Val Ala Leu Val Lys Gly Asp Val Asn Thr Ala Val  
 595 600 605

Asn Ala Ala Thr Val Ala Val Glu Asn Asn Ser Leu Leu Ala Arg Arg  
 610 615 620

Arg Val Asn Ile Arg Trp Thr Pro Arg Gln Glu Leu Glu His Glu Tyr  
 625 630 635 640

Ala Ile Leu Glu Ile Gln Ala Ile Thr Asn Gln Ile Arg Arg Leu Asp  
 645 650 655

Pro Lys Phe Asn Gly Ile Ala Ile Leu Arg Thr Pro Gly Glu Pro Trp  
 660 665 670

Thr Arg His Asp Val Gln Thr Tyr Arg Gln Tyr Tyr Asn Gln Leu Arg  
 675 680 685

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Glu Ser Arg Gly Phe Ala Val Glu Pro Ile Tyr Arg Ile Arg Ile Asn  
 690 695 700

Asn Gly Asn Glu Phe Asn Arg Ile Met Ser Ser Lys Tyr Pro Tyr Asn  
 705 710 715 720

Glu Leu Tyr Val Ala Asn Pro Lys Ser Ala Thr Gly Tyr Phe Arg Val  
 725 730 735

Asp Ser Tyr Asp Pro Ala Thr Arg Glu Ile Ile Ser Arg Lys Phe Thr  
 740 745 750

Gln Phe Ser Gln Ile Gln Glu Ser Thr Gly Ile Gly Tyr Ile Lys Glu  
 755 760 765

Ala Val Arg Lys Tyr Ser Pro Gly Thr Val Ile Ser Asn Val Pro Ser  
 770 775 780

Thr Pro Thr Thr Ile Arg Gly Arg Lys Leu Glu Gly Lys Leu Ile Leu  
 785 790 795 800

Glu Val Pro Ala Gln Val Asn Pro Ile Pro Gln Ser Val Leu Arg Ala  
 805 810 815

Ala Gln Glu Glu Asn Val Ile Ile Arg Asp Thr Thr Gly Arg Ile Tyr  
 820 825 830

Lys

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met	Lys	Lys	Asp	Ile	Phe	Tyr	Cys	Glu	Gln	Trp	Ser	Tyr	Gly	Tyr	Lys	1	5	10	15
Arg	Leu	His	Lys	Pro	Phe	Ser	Glu	Lys	Gln	Ala	Glu	Glu	Lys	His	Leu	20	25	30	
Lys	Gly	Glu	Leu	Tyr	Thr	Ala	Val	Ile	Gly	Ser	Ala	Thr	Gln	Pro	Glu	35	40	45	
Tyr	Val	Ile	Thr	Leu	Arg	Glu	Glu	Val	Gly	Phe	Phe	Ser	Val	Asn	Phe	50	55	60	
Phe	Asp	Lys	Phe	Gly	Arg	Asp	Tyr	Leu	Thr	His	Gln	Phe	Gln	Lys	Tyr	65	70	75	80
Ser	Asn	Ser	Asn	Tyr	Tyr	Phe	Leu	Ser	Met	Ala	Val	Trp	Arg	Asp	Tyr	85	90	95	
Ile	Thr	Leu	Glu	Ser	His	Asp	Leu	Ala	Glu	Gly	Tyr	Thr	Tyr	Phe	Phe	100	105	110	
Asn	Glu	Asn	Thr	Asp	Asp	Cys	Tyr	Val	Leu	Lys	Gln	Asp	Phe	Ile	Asn	115	120	125	
Asn	Glu	Arg	Tyr	Glu	Lys	Thr	Glu	Leu	Tyr	Ser	Gln	Lys	Asp	Lys	Val	130	135	140	



Ile Leu Phe Pro Lys Phe Gly Glu Tyr Asp Leu Val Leu Asn Pro Asp  
 145 150 155 160

Ile Ile

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Met Asn Lys Arg Met Lys Met Cys Pro Ala Cys Gln Gln Gly Tyr Leu  
 1 5 10 15

Tyr His Ser Lys Pro Lys Tyr Leu His Asp Glu Ile Ile Leu Cys Asp  
 20 25 30

Glu Cys Asp Ala Val Trp Leu Lys Gly Met Asn Ile Phe Tyr Gly Glu  
 35 40 45

Tyr Glu Lys Asp Phe Tyr Ser Tyr Val Pro Phe Met Glu Ser Gln Gly  
 50 55 60

Ile Thr Ser Glu Cys Ile Trp Glu Gly Asp Leu Phe Asp His Pro Tyr  
 65 70 75 80

Tyr Glu Asp Glu Asn Ser Asn Asp Met Asp

85

90

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Ala Thr Glu Ile Glu Lys Ala Lys Ala Lys Ile Thr Ala Tyr  
1                      5                      10                      15

Ser Lys Leu Val Ala Gly Thr Ala Ser Ala Val Val Gly Gly Asp Val  
20                      25                      30

Asn Thr Ala Ala Asn Ala Ala Gln Ile Ala Val Glu Asn Asn Thr Leu  
35                      40                      45

Tyr Pro Arg Cys Val Gly Ala Lys Cys Asp Glu Phe Gln Lys Glu Gln  
50                      55                      60

Gln Lys Trp Ile Arg Glu Asn Pro Glu Glu Tyr Arg Glu Val Leu Leu  
65                      70                      75                      80

Phe Gln Thr Gly Phe Ile Pro Ile Ile Gly Asp Ile Gln Ser Phe Val  
85 90 95

Gln Ala Gln Thr Ala Ala Asp His Leu Phe Ala Leu Leu Gly Val Val  
100 105 110

Pro Gly Ile Gly Glu Ser Ile Gln Ala Tyr Lys Val Ala Lys Ala Ala  
115 120 125

Lys Asn Leu Gln Gly Met Lys Lys Ala Leu Asp Lys Ala Ala Thr Val  
130 135 140

Ala Thr Ala Gln Gly Tyr Val Ser Lys Thr Lys Ile Lys Ile Gly Gln  
145 150 155 160

Thr Glu Leu Arg Val Thr Ala Ala Thr Asp Lys Gln Leu Leu Lys Ala  
165 170 175

Ile Gly Glu Gly Arg Asp Thr Thr Gly Lys Met Thr Glu Gln Leu Phe  
180 185 190

Asp Ser Leu Ala Lys Gln Asn Gly Phe Arg Val Leu Ser Gly Gly Lys  
195 200 205

Tyr Gly Gly Asn Asn Gly Phe Asp His Val Trp Gln Ala Ala Asp Gly  
210 215 220

Ser Val Val Leu Ile Val Glu Ser Lys Gln Ile Arg Asn Gly Thr Val  
225 230 235 240

Gln Leu Asn Pro Asn Gly Ala Gly Gly Tyr Thr Gln Met Ser Glu Asp  
245 250 255

Trp Ile Arg Gln Val Leu Asp Gln Leu Pro Asp Gly Ser Pro Ala Lys  
260 265 270

Ala Ala Val Phe Lys Ala Asn Lys Asn Gly Thr Leu Lys Thr Ala Ile  
275 280 285

Ala Gly Val Asp Arg Gln Thr Gly Lys Ala Val Ile Leu Pro Val Lys  
 290 295 300

Val Pro Ser Lys Thr Asn Ile Arg Arg  
 305 310

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Met Gly His Asn Met Met Thr Thr Gln Lys Trp Tyr Glu His Ile Thr  
 1 5 10 15

Asn Val Ile Ile Gly Asn Thr Ala Asn Phe Asn Ser Gly Cys Leu Asp  
 20 25 30

Ser Ile Asp Tyr Val Asp Glu Arg Lys Gly Val Pro Leu Ala Ala Met  
 35 40 45

Gln His Ile Phe Met Asp Val Arg Ala Ala Ala Ser His Ala Tyr Leu  
 50 55 60

Phe Glu His Asp Leu Lys Lys Phe Lys Gln Tyr Ala Tyr Val Ala Gly  
65 70 75 80

Lys Leu Gly Val Leu Leu Ser Val Asn Ser Thr Asp Pro Glu Pro Phe  
85 90 95

Phe Phe Pro Cys Asp Met Leu Asn Ile Gln Asn Pro Met Phe Leu Met  
100 105 110

Leu Met Ser Asp Ser Pro Gln Leu Arg Glu Phe Leu Val Arg Asn Ile  
115 120 125

Asp Asn Ile Ala Asn Asp Thr Glu Ala Phe Ile Asn Arg Tyr Asp Leu  
130 135 140

Asn Arg His Met Ile Tyr Asn Thr Leu Leu Met Val Glu Gly Lys Gln  
145 150 155 160

Leu Asp Arg Leu Lys Gln Arg Ser Glu Lys Val Leu Ala His Pro Thr  
165 170 175

Pro Ser Lys Trp Leu Gln Lys Arg Leu Tyr Asp Tyr Arg Phe Phe Leu  
180 185 190

Ala Phe Ala Glu Gln Asp Ala Glu Ala Met Lys Ala Ala Leu Glu Pro  
195 200 205

Leu Phe Asp Lys Lys Thr Ala Arg Met Ala Ala Lys Glu Thr Leu Ser  
210 215 220

Tyr Phe Asp Phe Tyr Leu Gln Pro Gln Ile Val Thr Tyr Ala Lys Ile  
225 230 235 240

Ala Ser Met His Gly Phe Asp Leu Gly Ile Asp Gln Glu Ile Ser Pro  
245 250 255

Arg Asp Leu Ile Val Tyr Asp Pro Leu Pro Ala Asp Glu Tyr Gln Asp  
260 265 270

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Ile Phe Asp Phe Met Lys Gln Tyr Asp Leu Ser Tyr Pro Tyr Glu Tyr  
 275 280 285

Leu Gln Asp Trp Ile Asp Tyr Tyr Thr Phe Lys Thr Asp Lys Leu Val  
 290 295 300

Phe Gly Asn Ala Lys Arg Glu  
 305 310

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCCACCGGTA CGGAAACTGA A

21

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CCTGAATTCA TGTCTATTCC ATTTTGAAGA

30

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CCGAGATCTT TAACCCTTTG GGCTTAAGCG A

31

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single

09928457.081404  
104180.262660

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GGGAGATCTC CCGCTCGTGT TGTGCATTA

29

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

AAGAGATCTG CAGCCAAGGC TCTCGAAA

28

(2) INFORMATION FOR SEQ ID NO: 51:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GGGAGATCTC AGGCTGCCGC CGTTGA

26

## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGGAGATCTC ACCCCAAGAA CGCCAAAA

28

## (2) INFORMATION FOR SEQ ID NO: 53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGGAGATCTG AACGTATAGT AATCTATCCA A

31

## (2) INFORMATION FOR SEQ ID NO: 54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

AGTGGCTCCT AG

12

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## (2) INFORMATION FOR SEQ ID NO: 55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

AGCACTCTCC AGCCTCTCAC CGAG

24

## (2) INFORMATION FOR SEQ ID NO: 56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

AGTGGCTCTT AA

12

## (2) INFORMATION FOR SEQ ID NO: 57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

AGTGGCTGGC

10

## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AGCACTCTCC AGCCTCTCAC CGAC

24

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs

- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GTACTTGCCT AG

12

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACCGACGTCG ACTATCCATG AACG

24

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GTACTTGCTT AA

12

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GTACTTGGGC

10

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

00928457 "001401  
101100" 25482660

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGACGTCG ACTATCCATG AACC

24

(2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

AATTCTCCCT CG

(2) INFORMATION FOR SEQ ID NO: 65

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGGCAACTGT GCTATCCGAG GGAG

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GATCAACTTT TCCCTGTTTG TCCCATTACC GGTTTGAATG AACCGATTGC GCGCCGCGCG 60

TGTTGTTGGA CATTACCTGC GATTCAGACG GTACGATTGA CCACTACATC GAGGAGAACG 120

GCAATCAGGG TACAATGCTA 140

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GATCCGCGTA CTTGGTTTTT CATATTTTGC ATAGTCTTGT CGGTCGGGCA TCTTCCCCGA	60
CATCATCTAA ATTTGTCTTT ATTGGTTTTT ACGCCACTCA TTGCGGATAA ACAATATTCC	120
GCCTTGCCGT CGCGAATGTT CAAGCTAGCC TGCATCACC G TAATCAGGTT GCCCGTTACC	180
GAGCCTTCGA GA	192

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GATCCGGCTG CCCGACGCGC GCAAAATTGC CGCCGAGGAA AGCGCGCACA ACCACGACGG	60
CAAAACCAGC GTATGGCAAT ACAAACATCT CGTGTTCGGT ACGGCAGGCA TTTTCTGCTA	120
TGTCGGCGCG GAGGTGTCTA TCGGTTCGTT GATGGTCAAC GTATTGGGTT ATCTGAAAGG	180
GCTGGATC	188

## (2) INFORMATION FOR SEQ ID NO: 69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GATCCCCCAC TTTACCTCGG GCAGATTTTG CGCGTTCATT ACAATAGCGT ATTTATGCGT	60
TTGCGTTTGC GCTTGCCGCT GCGCGGATATG GGAAAACATC AATATGGCGG	120
TATAAAGCGC GGTATGGCGG AAAACCTGCC GTTCCAAGT TTTATTCATC TTTTATTCCT	180
TGAGTTTGCC TTCACGGGAC GGGGCGGCGC GCGGAACGCG GGGTTCGGTA AACCGCCCGA	240
TTCCGCGCCC GCCGAATTGC TGATTGAAAA GCTTACTTCC CCATTTTAAC TTTGCACACT	300
GATC	304

## (2) INFORMATION FOR SEQ ID NO: 70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GATCAGACCC ATTTTCAGCG CACCGTAAGC GCGGATTTTC TCGAATTTTT CCAAAGCTGC	60
GGCATCGTTG TTGATGTCGT CTTGCAACTC TTTGCCCGTG TAGCCCAAGT CGGCGGCATT	120
CAGGAAAACG GTCGGAATGC CCGCGTTGAT GAGCGTGGCT TTCAAACGGC CTATATTCGG	180
CACATCAATT TCATCGACCA AATTGCCGGT TGGGAACATA CTGCCTTCGC CGTCGGCTGG	240
ATC	243

(2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CGGCGGCGTAGTccgccGcgACAGCGTTACCATAAGCGGGACAGACTACACCCCTTTATCTAACCCGC  
 AAAGTTTGGATACGGAATTAAAATGGTTGCTTCAAGAAGCTCCCGAAATAGAAAATCCTTTTCGACCGC  
 GCCGTTTATCTCCATAATAATTTGGCGTATCTTCAATATTTTAAAGATTGCAATAAACGTACTGCCAG  
 AAAGTGCATGACCTTGTCGCTGATGCGCTCCG

## (2) INFORMATION FOR SEQ ID NO: 72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CGGTCAATCA CAAGAAAGTC AGCCGTCTGA TGGCGAAGAC GGGGCTGAAG GCAGTGATAT	60
GGCGGCGCAA ATACCGCTCG TTCAAAGGAG AAGTCGGCAA AATTGCGCCG AATATCCTGC	120
GACGCTGTTT CCATGCAGAA AAGCCGAATG AGAAATGGGT AACGGACGTT GCCGAGTTCA	180
ATGTAGGCGG AGAAAAGATA TACCTTTCTC CGATTATGGA TTTGTTTAAC GGGGAAATCG	240
TCAGTTACCG TATTCAGACC CGCCCGACTT TCGATTGGC	280

## (2) INFORMATION FOR SEQ ID NO: 73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

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CGGTGTTTTT CTTAACAATT CGCCGACTTC ATGGCGATAT TTAAGTGACA GTTGCTCCGC      60
CCACGCAGTT GCGCCGAAC CAGCACCACG ACATTATACT GATTATGCAC ATCGGCAAGA      120
TCAAAGTGAC CTATCGTAGT ATCGCAGACT GT                                     152

```

(2) INFORMATION FOR SEQ ID NO: 76

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

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CGGGAGGTTTTGTGCATCCTGATACCGATCGGTTGTTGTGCTCAAAGGACAGAAGGCCGCTGATAAA
CGAGATTACCTGTTTGTGCGCTATTGACGATTTTATACTCTGCCATTTTGCCAGACAAAACCGCAGAC
AGTGCTGCCAAGTTTCTGACCGAACATCTGGCCGACCCCTGCTTGACCTGATTGAGTACGCTTACTC
TGACAATGATAGGTAATATAAAGAGCCGTCCAACATGCTTTCGGTGACGTTTGTTATGATAATGGGAT
TGGTTGGAGGCTTGCCCGATTTGCTTGTCGCGACCAACGGTAAGGCGGAGCGGGTTATCCGTACCT
TGATGGAGATGTGGCATGAGGAACAGTCGTTTGACAGACCG

```

(2) INFORMATION FOR SEQ ID NO: 77

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CGGAGCATAA AATCGTTATT AAAGATAATG GTATAGGAAC GAGCTTCGAT GAAATCAATG	60
ATTTTTATTT GAGAATCGGT CGGAACAGAA GGGAAGAAAA ACAAGCCTCC CCGTGCGGAA	120
GAATTCCAAC GGGTAAAAAA GGCCTTGTA AATGGCATT ATTGGGCTT GGCAACAAAA	180
TTGAAATTC TACTATCCAG GGAAACGAAA GGGTACTTT TACTTTGGAT TATGCAGAGA	240
TTCGAAGAAG CAAGGGTATT TATCAACCG	269

## (2) INFORMATION FOR SEQ ID NO: 78

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CGGATGAAAACGGGCATACGCgcCAAAGTATTTACGAACATCAaAGGCTTGAAGATACCGCACACCTAC  
 ATAGAAACGGACGCGAAAAAGCTGCCGAAATCGACAGATGAGCAGCTTTCGGCGCATGATATGTACGA  
 ATGGATAAAGAAGCCCGAAAAATATCGGGTCTATTGTCATTGTAGATGAAGCTCAAGACGTATGGCCG

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

CGGTTTCAGG TTGTCGCGAA GGCTCGGTAA CGGGCAACCT GATTACGGGT GATGCAGGCA	60
GCTTGAACAT TCGCGACGGC AAGGCGGAAT ATGTTTATCC GCAATGAGTG GCGTAAAAAC	120
CAATAAAGAC AAATTTAGAT GATGTCGGGG AAGATGCCCC ACCGACAAGA CTATGCAAAA	180
TATGAAAAAC CAAGTACGCG GATCAGGCAT GGATGCACGA TCCAATCCG	229

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG TTTGGAAATA	60
TTGTGTATCG GGGGGGGGTA TTTGCTGACG TAAAAACTA TAAACGCCGC GCAAAATATG	120
GCTGACTATA TTATTGACTT TGATTTTGTG CTGCGCGGTG ATGGATAAAA TCGCCAGCGA	180
TAAAGAATTT GCGAGAACCT GATGCCG	207

(2) INFORMATION FOR SEQ ID NO: 81 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CGGCAACGAT TTGAGCTATC GCGGTTACGA CATTCTGGAT TTGGCACAAA AATGCGAGTT	60
TGAAGAAGTC GCCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC	120
TTATAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTGGGA	180

AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG

224

## (2) INFORMATION FOR SEQ ID NO: 82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CGGGAACAGC CATTGCCCAC GCCCACGCCC CCCAAGAAAG ACGGAACTA CTGCCTAAAT	60
TTTCGGCAAT CAAGTTGACG ATTAAAGGGT TGGGGGCAGT TGCAGTAATA AACATAGCCG	120
ACGAAATGGG ATTGGAATGA TAGTTGACCA AAGCCAAATA TTTACCCATC TTGCCTTCTG	180
TGCCTTTTGC GGGATTGGAG CCGTAACTGC CG	212

## (2) INFORMATION FOR SEQ ID NO: 83

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

CGGGAATTCT GAGCAGAATG AAAGAAAGCA GGCTTGATAA TTTCATAAAG TTATTGGAAG	60
AAAAAGGATT TACCGTCCAT TTCGGTATTC ACAATACGGC TGATTACGGA ATTCCCCAAA	120
GCCGTAAAAG ATTTACGTTA ATTGCAAACA GAATAACCAA AGAAAAGCTG GAACCAGTCA	180
AGTATTCGGG CAAACGGCTT ACGGTAGCCG ATGTTTTGGG AATGGAAATG GCTTTCCCAA	240
CATTATTGCA GGACACCAAG ACGAAACGGA TTTTATGCAT AGCTGTGCGG GAATTATCTG	300
ATATCACTTG AACGATTGGC TTGATACCTA AAAACGGAGG AACCGTTGGC TTT	353

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AATTCGTAT CCAAACCTTG CGGGTTAGAT AAAGGGGTGT AGTCTGTCCC GCTTATGGTA	60
ACGCTGTGCG GCGGACTAC GCCCGGAGCC TTTTCCAGT AAGTTTTCGG AAATCAGGCT	120
GTGGGTGGTT TTTAAGAAAT CCAACCAGTC AAACGGCTCG GGGCTGTCCA AACCGGACAC	180

AGGTGCCGGT AACTTTCCCT CAGGTTGATT AACATTACGG CATCCGAATA TAACTTCCCG 240  
 CCTGCGGTTT GCCCGAGTTT AAGCAATGCC TCGTATCGT ATTGATTATA AAGTGTTTCC 300  
 TTCCAATT 308

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AATTCGTGTG CCGCGTCGAC AAACCGCTGA CGTAGCGGAT GTTCATGCC ACGTTTCAAA 60  
 GCAGGTTGAT GGCGGTTAGC AACCTCTGA TTCACTGGG ATAT 104

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

AAATTGCGTAG AGTGGGCTTC AGCCACGTTT TTTCTTTTTC GGTCGTTGAT TGGTGGGCTG 60

AACCACTTGT TTCGGAAATC CGTATCATG 89

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AATTTCCACC TATGCCCTAC GCAGCGATTA TCCGTGGTTT ACCCAAAGGG TGATTATGGC 60

AAAAGCGCGG GGTGAGCGA CCGCCTTTTG TTGCCGGCGT TCAAACGGGT TTTGATAGGA 120

AATGCAGGCA CGAAGCCTCG GCTGATTGTG ATGCACCTGA TGGGTTCGCA CAGTGATTTT 180

TGCACACGTT TGGATAAGGA TGC GCGGCGG TTT CAGTATC AA ACTGAAAA AATATCCTGC 240

TATGTTTCCA TCAATCGCGC AAACCGATAA ATT 273

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

AATTCTTCCG CACGGGGAGG CTTGTTTTTC TTCCCTTCTG TTCCGACCGA TTCTCAAATA	60
AAAATCATTG ATTTTCATCGA AGTTCATTCC TATACCATTA TCTTTAATAA CGATTTTATG	120
CTCCGGTTTA TCGAATAACC TAACTTCCAC TTCCGTAGCA CATGCATCGT AGGCATTTCG	180
TATCAACTCG GCAATCGCAG GAACAGTGTG CGAATACAAT CTTTACACCC AAATGTTTCGA	240
TTACGGTTGG CTCGAAACTC AATTTC AATT	270

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

AATTATGAAC ACACGCATCA TCGTTTCGGC TCGTTTCGTT GCGTTGGCAT TAGCAGGTTG 60  
 CGGCTCAATC AATAATGTAA CCGTTTCCGA CCAGAACTT CAGGAACGTG CCGCGTTTGC 120  
 CTTGGGCGTC ACCAATGCCG TAAAAATCAG CAACCGCAGC AATGAAGGCA TACGCATCAA 180  
 CTTTACCGCA ACTGTGGGTA AGCGCGTGAC CAATGCTATG TTACCAGTGT AATCAGCACA 240  
 ATCGGCGTTA CCACTTCCGA TGCAATT 267

## (2) INFORMATION FOR SEQ ID NO: 90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

AATTTTTATT TGGTTCGTAG TCATTTTGTG CAACTGAACG ATATTCGTTT TCATCATTGC 60  
 TAACGTCTAG TGCCCATTGT GGCCCGTAAT AAGAGATTTC GTCTCCTTTT ACATGTTTGA 120  
 CGCTGACGGC ATACTGGGGA TCGATGACGG ATAATGTACG TCTGTTGACA TCTGCAACGC 180  
 TAAATCAATC ATCGGTATTG GATAATGCGT TGCCGATGTT TTGACTTGTA TGTT 234

## (2) INFORMATION FOR SEQ ID NO: 91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs

- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AATTCGGCCG GCTGTGTCAA ATAATGCGTT ACTTTGGCCG GGTCTTGTTT TTTGTAAGTG	60
GTGGTCTTTT TTTGCGCGTT ATCCCCATCT GTTTGAGTGC ATAGCAAATG GTGGCTGCCG	120
TACAATCAAA TGTTTGGCGT TCATGCAGAT AGGCATCATG GTGTTGCCCA ATATATTGAG	180
CCGGTTTTTTG CCTATCCGAT TTGACGGCAT TTAGACCGGT AACTTGATGT TTTAAGCTGC	240
CTGTTTGTTT AAAGGCGAAT CCACAAGTAA AGCGTGTTTC TTGACAGGTT AAACG	295

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:



AATTGTGTAT ATCAAGTAGG ATGGGCATTT ATGCCTGACC TACAAAACCA AAAACAACCT 60  
 ACCACCCTTA ATCAACTCCA CAAACCCTCT TCAGACAACC TCGTTTTTTTG AAAACAATC 120  
 TGTAAACAGA TAACTGCTGA AGAATACCGT TGCCGAGCCC CAAAACCCGT ACTGCAACTT 180  
 TTATTGTGAA CTTCCCATTA TGAGAAAATC CCTTTTCGTC CTCTTTCTGT ATTCGTCCCT 240  
 ACTTACTGCC AGCGAAATT 259

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

AATTGCACCA CGCGATGATG GGTACGCCTC TGTTGCCATT GCGACCGCCG CCGCCGTGCC 60  
 CGGTACGCTG GTCAACCTTG CCGCGGCGGA ACGGGTAAAG AAGTGCGCTT CGGGCATCCT 120  
 TCCGGTACAT TGC GCGTCGG TGCAGCGCCG AATGTCAGGA CGGACAATGG ACGGCCACCA 180  
 AAGCGGTTAT GAGCCGCAGC GCACGCGTGA TGATGGAAGG TTGGGTCAGG GTGCCGGAAG 240  
 ATTGTTTTTA AATTGGACGG CGAACCGGTC TATTCGTATT GCGGTTATAC CGCCGCAAAG 300  
 GCAGACCTTG AAACCTGGTGC GTGCCGTGCA GGGCATGTAC GGCTATGTGT GCGTGCGGGG 360

CGGATTTGAT GTGCGGAAT

379

## (2) INFORMATION FOR SEQ ID NO: 94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AATTTGTTGG GCAGATGGCC GTGAATCAGC AGGTGGGCGA CTTCTTCAAA CTCGCATTTT	60
TGTGCCAAAT CCAGAATGTC GTAACCGCGA TACGTCAAAT CGTTGCCGGT ACGCAACGGT	120
ACACAAAGCG GTATTACCGG CCGCAACGCC AGAAAGCGCA ACGGATTTTT AGGTTTGAGG	180
GTCGGGGTTT GAGTAGTTTC AGTCATGGTA TTTCTCCTTT GTGTTTTTAT GGGTTTCGGG	240
TTTTCAGACG ACCGATGCGG ATTTGTTGAA AGGCAGTCTG AAAGCGGTAA ATCATTTTTG	300
AAACAATT	308

## (2) INFORMATION FOR SEQ ID NO: 95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AATTCGGAGG AGCAGTACCG CCAAGCGTTG CTCGCCTATT CCGGCGGTGA TAAAACAGAC	60
GAGGGTATCC GCCTGATGCA ACAGAGCGAT TACGGCAACT TGTCTACCA CATCCGTAAT	120
AAAAACATGC TTTTCATTTT TTCGGCAAGC AATGACGCAC AAGCTCAGCC CAACACAACT	180
GACCTATTG CCATTTTATG AAAAAGACGC TCAAAAAGGC ATTATCACAG TTGCAGGCGT	240
AGACCGCAGT GGAGAAAAGT TCAATGGCTC CAACCATTGC GGAATT	286

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AATTTGGATA CGTTGGAAAA GGGATATTTG ATTGGGAATG GGATGAAGAT AAGCGTAGAT	60
GAGTTGGGGA AAAAAGTGTT AGAACATATC GGTAAGAATG AACCGTTATT GTTGAAAAAT	120

CTACTGGTTA ACTTCAATCA GGGAAAACAT GAAGAAGTTA GGAAGTTGAT TTATCAGTTG 180  
 ATAGAGTTAG ATTTTCTGGA ACTTTTGTGA GGGATTCTAT GAAAAACTGG AAGCAATT 238

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AATTCGGCAC GCAGGTTTTT TAAAAAAGG CCGTTGATGA CTTTGTGAT ATTGGCGGCT 60  
 TCGGTGTAGT GCGCGCCCGC TTCGGCCGCT CTTGCGCGTC CATGACGGAT TGGAAGAGCG 120  
 TGCCGAAGAT TTCTGGACTG ATGTTGCGCC AGTCGAAATT GCCGACACGG GAGGAATACC 180  
 TGCCAACAAG AGTGCAGGCA GCGTAATCAA ACCACCCCCA CCCGCAATCG CATCGATAAA 240  
 TCCGGCAATC ATCGCAACCA AACCCAAAGC GAGTATTATG TATAAATCTT CCATGTTTCT 300  
 TAATCCTGTT AACTGCACC AA 322

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

AATTTGTCGG CAATCTTCCC GGGTCGCTTT ATTTTGTGCA GGCATTATTT TTCATTTTGG	60
GCTTGACAGT TTGGAGATAT TGTGTATCGG GGGGGGGTAT TTGCTGACGT AAAAAACTAT	120
AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC CTGCGCGGTG	180
ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG ATGCCGGCCT GTTGTTGAAT	240
ATTTTCGACC TGTAATTACG ATTTGGCTTC CGCGCCGGCA CAATATGCCG CCAAGCGGCG	300
CCCACATTTT GGAAGC	316

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

AATTCGGACA GTATGAATAC AGCGGATTAA TACAAGGTAA GTTCATTACA ACGGAAAAAC	60
CTTTAAAGAA TAATATGAAA GGTATTACCT TGTTTGCCAA CGGGAATGGT AAATATGCCC	120
GAGTTTTTCA CTGAATAGCG AATCCAGCCA TTTCTATTCA TATTTGACTG GATGGCTGAA	180
TGTGGACTTT ATAGATAATG ACGATGAAGA TTTAATT	217

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